



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 138608

To: Sarvamangala Devi  
Location: REM 3C18  
Art Unit: 1645  
Tuesday, November 23, 2004  
  
Case Serial Number: 10/022832

From: Beverly Shears  
Location: Remsen Bldg.  
RM 1A54  
Phone: 571-272-2528  
  
beverly.shears@uspto.gov

### Search Notes

Shears, Beverly

From: Devi, Sarvamangala  
Sent: Tuesday, November 23, 2004 7:39 AM  
To: Shears, Beverly  
Subject: 10/022,832

Beverly:

In application 10/022,832, would you please perform a sequence search for SEQ ID NO: 2 in commercial and interference databases? Please include an inventors' name search for France Couture; Josee Hamel; Bernard R. Brodeur; Denis Martin; Pascal Brassard; Frederic Beaudoin; and Paul Prefontaine.

Thanx.

S. DEVI, Ph.D.  
AU 1645  
Rems - 3C18

Searcher: Beverly e 2528

Terminal time: \_\_\_\_\_

Elapsed time: \_\_\_\_\_

CPU time: \_\_\_\_\_

Total time: \_\_\_\_\_

Number of Searches: \_\_\_\_\_

Number of Databases: \_\_\_\_\_

\_\_\_\_\_ STIC

\_\_\_\_\_ CM-1

\_\_\_\_\_ Pre-S

#### Type of Search

\_\_\_\_\_ N.A. Sequence

\_\_\_\_\_ A.A. Sequence

\_\_\_\_\_ Structure

\_\_\_\_\_ Bibliographic

\_\_\_\_\_ IG

☒ STN

☒ Dialog

\_\_\_\_\_ APS

\_\_\_\_\_ Geninfo

\_\_\_\_\_ SDC

\_\_\_\_\_ DARC/Questel

\_\_\_\_\_ Other

**This Page Blank (uspto)**

---

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 12:10:53 ; Search time 154 Seconds

(without alignments)  
600.988 Million cell updates/sec

Title: US-10-022-832-2

Perfect score: 1299

Sequence: 1 MNRRLNVLATVALSVAS.....LIQASDEVAAPVQGNQGE 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1299	100.0	258	2	AAY35281 Chlamydia
2	1299	100.0	258	3	AAY56993 C. pneumo
3	1299	100.0	258	5	ABB90553 Chlamydia
4	1299	100.0	258	5	ABP61993 C. pneumo
5	1250	96.2	249	3	AAY56994 C. pneumo
6	763	58.7	243	7	ADD43854 Chlamydia
7	744	57.3	250	2	AAY37675 Chlamydia
8	305.5	23.5	249	6	ADA34321 Acinetoba
9	297	22.9	272	3	AAY75136 Neisseria
10	297	22.9	272	3	AAY75787 Neisseria
11	297	22.9	272	3	AB25632 N. mening
12	297	22.9	272	3	AB58562 N. mening
13	287.5	22.1	269	3	AB25631 N. mening
14	287	22.1	272	3	AAY75786 Neisseria
15	287	22.1	272	3	AAY75137 Neisseria
16	287	22.1	272	3	AAY75789 Neisseria
17	287	22.1	272	3	AAY75134 Neisseria
18	287	22.1	272	3	AB25631 N. mening
19	287	22.1	272	3	AB58564 N. mening
20	287	22.1	272	3	AB58561 N. mening
21	285	21.9	272	3	AAY75135 Neisseria
22	285	21.9	272	3	AAY75788 Neisseria
23	285	21.9	272	3	AB25633 N. gonorr
24	285	21.9	272	3	AB58563 N. gonorr
25	285	21.9	334	6	ABP77252 N. gonorr

26	284	21.9	272	3	AAB25634 N. mening
27	282.5	21.7	269	3	AAY82950 BAS023 p
28	279.5	21.5	222	3	AAY75133 Neisseria
29	279.5	21.5	222	3	AAY75784 Neisseria
30	279.5	21.5	222	3	AAB25629 N. mening
31	279.5	21.5	222	3	AAB58559 N. mening
32	269.5	20.7	255	6	ABM70454 Phototab
33	263	20.2	323	7	ABO69153 Pseudomon
34	262.5	20.2	215	3	AAY75132 Neisseria
35	262.5	20.2	215	3	AAY75785 Neisseria
36	262.5	20.2	215	3	AAB25630 N. gonorr
37	262.5	20.2	215	3	AAB58560 N. gonorr
38	253	19.5	246	6	ADA34326 Acinetoba
39	237	18.2	254	7	ABO64397 Klebsiell
40	233.5	18.0	255	7	ADF06499 Bacterial
41	233.5	18.0	270	8	ABM79751 Expresgio
42	233.5	18.0	270	8	ADO14134 Chaperone
43	233	17.9	385	6	ABP71560 Fkpa-gp21
44	233	17.9	537	6	ABP72251 Single ch
45	233	17.9	688	6	ABP71559 FkpApkpAg

## ALIGNMENTS

## RESULT 1

AAY35281  
ID AAY35281 standard; protein; 258 AA.

AC AAY35281;

XX 17-OCT-2003 (revised)

DT 13-SEP-1999 (first entry)

XX Chlamydia pneumoniae transmembrane protein sequence.

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;  
KW neutralising epitope.

XX Chlamydophila pneumoniae.

XX WO9927105-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-IB001890.

XX 21-NOV-1997; 97FR-00014673.

XX 04-NOV-1998; 98US-0107078P.

XX (GEST ) GENSET.

XX Griffais R;

XX WPI; 1999-357842/30.

XX Genome sequence of Chlamydia pneumoniae.

XX Page 1103-1104; Disclosure; 1912pp; English.

XX AAY34584-Y35879 represent the proteins encoded by all the open reading  
frames in the complete genome (see AAY91990) of Chlamydia pneumoniae. C.  
pneumoniae causes respiratory disease such as pneumonia and bronchitis  
and is thought to be a contributing factor in heart disease, sarcoidosis,  
sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The  
polypeptides encoded by the open reading frames of the C. pneumoniae  
genome (see AAY34584-Y35879) can be used in immunogenic compositions as  
vaccines. Vectors containing C. pneumoniae nucleotide sequences can also  
be used as immunogenic compositions, especially where the vector directs  
the expression of a neutralising epitope of C. pneumoniae. (Updated on 17  
-OCT-2003 to standardise OS field)

CC	caused by C. pneumoniae. The present sequence represents the amino acid
CC	sequence of the C. pneumoniae full-length msp protein. (Updated on 12-SEP
CC	-2003 to standardise OS field)
XX	
SQ	Sequence 258 AA;
	Query Match 100.0%; Score 1299; DB 3; Length 258;
	Best Local Similarity 100.0%; Pred. No. 5.2e-118; Indels 0; Gaps 0;
	Matches 258; Conservative 0; Mismatches 0;
QY	1 MNRRNWLVLATVALALSVCDSVRSKDKQDQGLSVYKDKNDTNDIELSDNQLSRTFG 60
DB	1 MNRRNWLVLATVALALSVCDSVRSKDKQDQGLSVYKDKNDTNDIELSDNQLSRTFG 60
QY	61 HLLARQLRKSEDMFFDIAEVAKGLQAEELVCKSAPLTETEEYEEKVAEVLVFEKKSLENL 120
DB	61 HLLARQLRKSEDMFFDIAEVAKGLQAEELVCKSAPLTETEEYEEKVAEVLVFEKKSLENL 120
QY	121 SLAEKFLKENSKNAGVVEVQPSKLYKIIKEGAGKAISGKPSALLHYKGSFINGQVFPSS 180
DB	121 SLAEKFLKENSKNAGVVEVQPSKLYKIIKEGAGKAISGKPSALLHYKGSFINGQVFPSS 180
QY	181 EGNNEPILLPGQTIPGALGMOGMEGETRVLYIHPDLAYGTAGQLPPNSLLIFEINLI 240
DB	181 EGNNEPILLPGQTIPGALGMOGMEGETRVLYIHPDLAYGTAGQLPPNSLLIFEINLI 240
QY	241 QASADEVAAPVQEGNOGE 258
DB	241 QASADEVAAPVQEGNOGE 258
RESULT 3	
ABB90553	ID ABB90553 standard; protein; 258 AA.
XX	AC ABB90553;
XX	29-AUG-2003 (revised)
XX	29-JUL-2002 (first entry)
XX	Chlamydia pneumoniae cp6960 protein, SEQ ID NO:55.
DE	Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
XX	human respiratory disease; cardiovascular disease; atherosclerosis;
KW	coronary artery disease; carotid artery stenosis; myocardial infarction;
KW	cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW	strain CWL029.
XX	Chlamydia pneumoniae.
OS	Key Location/Qualifiers
XX	Key 1. .25
PH	Peptide /label= Signal_peptide
FT	FT 26. .258
FT	Protein /note= "Mature protein"
FT	
XX	WO200202606-A2.
EN	
XX	10-JAN-2002.
FD	
XX	03-JUL-2001; 2001WO-IB001445.
XX	
XX	03-JUL-2000; 2000GB-00016363.
PR	11-JUL-2000; 2000GB-00017047.
PR	11-JUL-2000; 2000GB-00017983.
PR	07-AUG-2000; 2000GB-00019368.
PR	18-AUG-2000; 2000GB-00020440.
PR	14-SEP-2000; 2000GB-00022583.
PR	10-NOV-2000; 2000GB-00027549.
PR	22-DEC-2000; 2000GB-00031706.
XX	(CHIR-) CHIRON SPA.
PA	
XX	

PI Ratti G, Grandi G;  
 DR WPI; 2002-154726/20.  
 DR N-PSDB; ABL91211.  
 XX  
 PT Novel Chlamydia pneumoniae protein useful in the manufacture of a  
 PT medicament for treatment or prevention of infection due to Chlamydia,  
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes.  
 XX  
 PS Claim 1; Page 69; 364pp; English.  
 PS  
 CC Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia  
 CC pneumoniae (strain CWL029), and ABL91184-ABL91173 represent DNA encoding  
 CC them. The proteins are predicted to be immunogenic and may therefore be  
 CC useful in vaccine production and for diagnostic purposes. Chlamydia  
 CC pneumoniae is a common cause of respiratory disease in humans, and is  
 CC also involved in the development of cardiovascular diseases such as  
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,  
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,  
 CC claudication and stroke. The proteins and nucleic acids of the invention  
 CC may be used in vaccines and pharmaceutical compositions for the  
 CC prevention or treatment of chlamydial infections, particularly Chlamydia  
 CC pneumoniae infections. The proteins may also be used in the detection of  
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched  
 CC DNA probe assay or blotting techniques for determining Chlamydia  
 CC pneumoniae gene expression. The present sequence represents a  
 CC specifically claimed Chlamydia pneumoniae protein of the invention.  
 CC (Updated on 29-AUG-2003 to standardise OS field)  
 XX  
 CC Sequence 258 AA;  
 SQ  
 Query Match 100.0%; Score 1299; DB 5; Length 258;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-118;  
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNRWNLVATVALSASCDVRSKDKDQGSILVEYKDKNDTNDIELSDNQLSRFTG 60  
 DB 1 MNRWNLVATVALSASCDVRSKDKDQGSILVEYKDKNDTNDIELSDNQLSRFTG 60  
 QY 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVOKLVFEKSKENL 120  
 DB 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVOKLVFEKSKENL 120  
 QY 121 SLAEKFLKENSKNAGVVEVQPSKLYKIIEKGAGKAIKSGKPSALLHYKGSFINGQVFS 180  
 DB 121 SLAEKFLKENSKNAGVVEVQPSKLYKIIEKGAGKAIKSGKPSALLHYKGSFINGQVFS 180  
 QY 181 EGNNEPILLPLGQTTIPGFALGMOGKGEETRVLYIHPDLAYGTAGQLPPNLLIFEINLI 240  
 DB 181 EGNNEPILLPLGQTTIPGFALGMOGKGEETRVLYIHPDLAYGTAGQLPPNLLIFEINLI 240  
 QY 241 QASADEVAAPVQEGNQGE 258  
 DB 241 QASADEVAAPVQEGNQGE 258  
 RESULT 4  
 ID ABP61993 standard; protein; 258 AA.  
 XX  
 AC ABP61993;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 08-OCT-2002 (first entry)  
 XX  
 DE C. pneumoniae BVH-CPN1 from strain CWL-029.  
 XX  
 KW CWL-029; BVH-CPN; antibiotic; antibacterial; Chlamydial infection;  
 KW sinusitis; pharyngitis; bronchitis; pneumonitis; asthmatic bronchitis;  
 KW adult-onset asthma; chronic obstructive pulmonary disease; COPD;  
 KW atherogenesis; atherosclerosis.  
 XX  
 OS Chlamydophila pneumoniae.

XX Key Location/Qualifiers  
 FH Peptide 1..20  
 FT /label= Leader\_peptide  
 FT Protein 21..258  
 FT /label= Mature\_BVH-CPN1  
 XX EPI219635-A2.  
 XX 03-JUL-2002.  
 XX 21-DEC-2001; 2001EP-00130295.  
 XX 21-DEC-2000; 2000US-0256941P.  
 XX (SHIR-) SHIRE BIOCHEM INC.  
 PI Couture F, Hamel J, Brodeur BR, Martin D;  
 DR WPI; 2002-530680/57.  
 DR N-PSDB; ABQ92487.  
 XX  
 CC New Chlamydia pneumoniae proteins or antigens, useful for the  
 CC prophylactic or therapeutic treatment of Chlamydial bacterial infections,  
 CC e.g. sinusitis, pharyngitis, bronchitis, or chronic obstructive pulmonary  
 CC disease.  
 XX  
 CC Claim 9; Fig 2; 122pp; English.  
 XX  
 CC The invention relates to novel isolated polypeptides from Chlamydia  
 CC pneumoniae. The polypeptides of the invention have antibiotic and  
 CC antibacterial activity. The polypeptide or composition of the invention  
 CC is useful for the prophylactic or therapeutic treatment of Chlamydial  
 CC bacterial infection (specifically those caused by C. pneumoniae, C.  
 CC psittaci or C. trachomatis), e.g. sinusitis, pharyngitis, bronchitis,  
 CC pneumonitis, asthmatic bronchitis, adult-onset asthma, chronic  
 CC obstructive pulmonary disease (COPD), atherogenesis or atherosclerosis.  
 CC The sequences shown in ABP61993-ABP62011 represent proteins BVH-CPN1 to  
 CC BVH-CPN19 of C. pneumoniae. (Updated on 29-AUG-2003 to standardise OS  
 CC field)  
 XX  
 CC Sequence 258 AA;  
 SQ  
 Query Match 100.0%; Score 1299; DB 5; Length 258;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-118;  
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNRWNLVATVALSASCDVRSKDKDQGSILVEYKDKNDTNDIELSDNQLSRFTG 60  
 DB 1 MNRWNLVATVALSASCDVRSKDKDQGSILVEYKDKNDTNDIELSDNQLSRFTG 60  
 QY 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVOKLVFEKSKENL 120  
 DB 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVOKLVFEKSKENL 120  
 QY 121 SLAEKFLKENSKNAGVVEVQPSKLYKIIEKGAGKAIKSGKPSALLHYKGSFINGQVFS 180  
 DB 121 SLAEKFLKENSKNAGVVEVQPSKLYKIIEKGAGKAIKSGKPSALLHYKGSFINGQVFS 180  
 QY 181 EGNNEPILLPLGQTTIPGFALGMOGKGEETRVLYIHPDLAYGTAGQLPPNLLIFEINLI 240  
 DB 181 EGNNEPILLPLGQTTIPGFALGMOGKGEETRVLYIHPDLAYGTAGQLPPNLLIFEINLI 240  
 QY 241 QASADEVAAPVQEGNQGE 258  
 DB 241 QASADEVAAPVQEGNQGE 258  
 RESULT 5  
 ID AAY56994 standard; protein; 249 AA.  
 XX  
 AC AAY56994;

```

XX 12-SEP-2003 (revised)
DT 08-MAY-2000 (first entry)
XX
XX C. pneumoniae mip (outer membrane protein) truncated protein.
DE
XX Chlamydia pneumoniae; outer membrane protein; mip; CPN100501;
KW Chlamydial infection.
XX
XX Chlamydia pneumoniae.
OS
XX WO200006741-A1.
XX
XX 10-FEB-2000.
XX
XX 27-JUL-1999; 99WO-IB001330.
XX
XX 27-JUL-1998; 98US-0094192P.
XX 01-MAR-1999; 99US-0122044P.
XX 26-JUL-1999; 99US-00361440.
XX
XX (CONN-) CONNAUGHT LAB LTD.
XX
XX Murdin AD, Oomen RP, Dunn PL;
XX
XX WPI; 2000-195302/17.
DR N-PSDB; AA256942.
XX
XX Novel polynucleotides and Chlamydia pneumoniae outer membrane protein
PT encoded by them for use as vaccines in treating and diagnosing chlamydial
PT infections.
XX
XX Claim 5; Fig 1A-C; 55pp; English.
XX
XX The invention provides an isolated polynucleotide encoding Chlamydia
CC pneumoniae outer membrane protein (mip or CPN100501). The mip protein can
CC be expressed by standard recombinant methodology. The mip gene is used
CC for detecting Chlamydia by hybridizing or amplifying the sample with the
CC mip gene specific probe. A vaccine vector or a pharmaceutical composition
CC comprising the mip gene are used for inducing an immune response in a
CC mammal to prevent/treat chlamydial infections particularly infections
CC caused by C. pneumoniae. The present sequence represents the amino acid
CC sequence of the C. pneumoniae truncated mip protein. (Updated on 12-SEP-
CC 2003 to standardise OS field)
XX
XX Sequence 249 AA;
SQ
Query Match 96.2%; Score 1250; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 3e-113;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRNRNLVATVALALSVASCDVRSKDKDQGSLEYKDKNDTNDIELSDNOKLRTFG 60
DB 1 MNRNRNLVATVALALSVASCDVRSKDKDQGSLEYKDKNDTNDIELSDNOKLRTFG 60
QY 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETEEYKMAEVQKLVFEKSKENL 120
DB 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETEEYKMAEVQKLVFEKSKENL 120
QY 121 SLAEKFLKSKNAGVVEQPSKLYKIIKEGAGKAIKSGKPSALLHYKGSFINGQVPS 180
DB 121 SLAEKFLKSKNAGVVEQPSKLYKIIKEGAGKAIKSGKPSALLHYKGSFINGQVPS 180
QY 181 EGNNEPILLPGQITPGFALGMOGKGETRVLVYHPDLAYGTAGOLPPNSLLIFEINLI 240
DB 181 EGNNEPILLPGQITPGFALGMOGKGETRVLVYHPDLAYGTAGOLPPNSLLIFEINLI 240
QY 241 QASADEVAA 249
DB 241 QASADEVAA 249

```

```

ADD43854
ID ADD43854 standard; protein; 243 AA.
XX
XX AC ADD43854;
XX
XX 15-JAN-2004 (first entry)
XX
XX Chlamydia trachomatis immunogenic protein, SEQ ID NO 149.
XX
XX immunogenic; infection; Chlamydia trachomatis; immune; vaccine;
KW gene therapy; antibacterial.
XX
XX Chlamydia trachomatis.
OS
XX WO2003049762-A2.
XX
XX 19-JUN-2003.
XX
XX 12-DEC-2002; 2002WO-IB005761.
XX
XX 12-DEC-2001; 2001GB-00029732.
XX 06-AUG-2002; 2002GB-00018233.
XX 14-AUG-2002; 2002GB-00018924.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Grandi G, Ratti G;
XX
XX WPI; 2003-532882/50.
DR N-PSDB; ADD43855.
XX
XX New immunogenic composition having a protein or encoding nucleic acid,
PT useful for diagnosing, preventing and/or treating Chlamydia trachomatis
PT infection.
XX
XX Claim 6; SEQ ID NO 149; 164pp; English.
XX
XX The invention relates to a novel immunogenic composition comprising a
CC protein or nucleic acid, and an adjuvant, where the protein or nucleic
CC acid comprises any of 131 fully defined amino acid or nucleotide
CC sequences given in the specification, or has 50% or greater sequence
CC identity to it, or their fragments. The protein and/or nucleic acid of
CC the immunogenic composition is useful in the manufacture of a medicament
CC for the treatment or prevention of infection due to Chlamydia
CC trachomatis. The infection is treated or prevented by the medicament
CC eliciting an immune response which is specific to a C. trachomatis
CC elementary body, or for neutralising C. trachomatis elementary bodies,
CC hence the immunogenic composition can be used in creating a vaccine. The
CC immunogenic compositions can also be used for the diagnosis of C.
CC trachomatis infection. The nucleic acids of the immunogenic compositions
CC can be used to treat disorders by gene therapy. The immunogenic
CC compositions have antibacterial activity. This sequence represents one of
CC the 131 C. trachomatis proteins with immunogenic properties of the
CC invention.
XX
XX Sequence 243 AA;
SQ
Query Match 58.7%; Score 763; DB 7; Length 243;
Best Local Similarity 61.1%; Pred. No. 9.8e-66;
Matches 149; Conservative 36; Mismatches 49; Indels 10; Gaps 2;
QY 5 WNLVLATVALALSVASCDVRSKDKDQGSLEYKDKNDTNDIELSDNOKLRTFGHLLA 64
DB 7 WMLMF---AVALPIVGC-----DNGGGSOTSATEKSMVEDSALTNDNOKLRTFGHLLS 56
QY 65 RQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETEEYKMAEVQKLVFEKSKENLSLAE 124
DB 57 RQLSRTEDFSLLVEVIKMGQSEIDQGSAPLTDTEYKMAEVQKASFEAKCSENLSAE 116
QY 125 KFLKSKNAGVVEQPSKLYKIIKEGAGKAIKSGKPSALLHYKGSFINGQVPSSEGN 184
DB 117 KFLKENKAGVIELEPNKLYRVVKEGTGRVLSCGKPTALLHYTGSFDGKRVFDSSEKNK 176

```

```
QY 185 EPILLPLGOTIPGPFALGMOGMEGETRVLVYHPDLAYGTAGOLPNSLLIPEINLIQASA 244
Db 177 EPILLPLTKVIPGFGMOGMEGEVRVLYIHPDLAYGTAGOLPNSLLIPEVKLIEAND 236
QY 245 DEVA 248
Db 237 DNVS 240

RESULT 7
ID AAY37675 standard; protein; 250 AA.
XX AAY37675;
AC AAY37675;
DT 07-OCT-1999 (first entry)
XX Chlamydia trachomatis surface exposed protein.
DE Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
KW bartholinitis; pneumonia; venereal lymphogranulomatosis.
XX Chlamydia trachomatis.
OS Chlamydia trachomatis.
XX WO9928475-A2.
PN 10-JUN-1999.
PD 27-NOV-1998; 98WO-IB001939.
XX 28-NOV-1997; 97FR-00015041.
PR 17-DEC-1997; 97FR-00016034.
XX 04-NOV-1998; 98US-0107077P.
PA (GEST ) GENSET.
PI Griffais R;
XX WPI; 1999-371125/31.
DR Genome sequence of Chlamydia trachomatis.
XX Disclosure; Page 1302-1304; 1755pp; English.
CC AAY36754-V37949 are encoded by open reading frames (ORFs) of the genome
CC of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as
CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
CC perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and
CC venereal lymphogranulomatosis. The polypeptides of the invention may be
CC of use in treating these diseases
XX Sequence 250 AA;
SQ

Query Match 57.3%; Score 744; DB 2; Length 250;
Best Local Similarity 60.2%; Pred. No. 7.3e-64;
Matches 147; Conservative 36; Mismatches 51; Indels 10; Gaps 2;
QY 5 WNLVLTVALALSVASCDVRSKDKQDQGLVYKDKNDTNDIELSDNOKLSRTFGHLLA 64
Db 14 WLMF---AVALPIVGC-----DNGGGSQTSATEKSMVEDSALTDNOKLSRTFGHLLA 63
QY 65 ROLRSEDMFFDIAEVAKQLQAEVLVCKSAPLTETETEYEEKMAEVQKLVPEKSKENLSLAE 124
Db 64 ROLRSEDFSLDVEIKGMQSEIDGQSAPLTDTTEYKMAEVQKASFEAKCSENLSAE 123
QY 125 KFLKENSKNAGVVEQPSKLYKIKKEGAKGAKSGKPSALLHYKSGFINGQVFSSEGN 184
```

```
Db 124 EFLKENKEKAGVIELEPNKQYRVVKEGTGRALSGKPTALLHYTGSFDGKDFDSEKNK 183
QY 185 EPILLPLGOTIPGPFALGMOGMEGETRVLVYHPDLAYGTAGOLPNSLLIPEINLIQASA 244
Db 184 AAILPLTKVIPGFGMOGMEGEVRVLYIHPDLAYGTAGOLPNSLLIPEVKLIEAND 243
QY 245 DEVA 248
Db 244 DNVS 247

RESULT 8
ID ADA34321 standard; protein; 249 AA.
XX ADA34321;
AC ADA34321;
DT 20-NOV-2003 (first entry)
XX Acinetobacter baumannii protein #1482.
DE Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
KW plant biocontrol agent.
XX Acinetobacter baumannii.
OS US5662958-B1.
PN 13-MAY-2003.
PD 04-JUN-1999; 99US-00328352.
XX 09-JUN-1998; 98US-0088701P.
PA (GENO-) GENOME THERAPEUTICS CORP.
XX Breton G, Bush D;
XX WPI; 2003-576092/54.
DR N-PSDB; ADA30195.
XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
PT for diagnosing a bacterial disease, as components of antibacterial
PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
PT plants.
XX Example; SEQ ID NO 5608; 328pp; English.
PS The invention relates to isolated Acinetobacter baumannii nucleic acids.
CC The A. baumannii nucleic acids and polypeptides are useful as reagents
CC for diagnosing a bacterial disease, as components of antibacterial
CC vaccines, as targets for antibacterial drugs, to detect the presence of
CC A. baumannii and other Acinetobacter species in a sample, in screening
CC compounds for the ability to interfere with the A. baumannii life cycle
CC or to inhibit A. baumannii infection, and as biocontrol agents for
CC plants. The present sequence represents the amino acid sequence of an A.
CC baumannii protein.
XX Sequence 249 AA;
SQ

Query Match 23.5%; Score 305.5; DB 6; Length 249;
Best Local Similarity 32.7%; Pred. No. 4.6e-21;
Matches 82; Conservative 45; Mismatches 87; Indels 37; Gaps 7;
QY 3 RRNVLVTVALALSV-ASCDVRSKDKQDQGLVYKDKNDTNDIELSDNOKLSRTFGH 61
Db 20 KKSIVIAASTMSLSVFAAAPITNKSPAKDQ-----FSSYGY 57
QY 62 LLARQLRKS-EDMFFDIAEVAKQLQAEVLVCKSAPLTETE-----YEEKMAEVQKLVPE 113
Db 58 LMGRNNTALTDLNLDI---FYQGLQEGAQNKARTUTDEEMAKAINDYKRTLEAKQLVFEQ 115
```





CC AA253015 to AA254536, AA254577 to AA254615, and AA254615 to AA254615  
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides  
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA254615 represent  
 CC PCR primers used in the exemplification of the present invention. The  
 CC polypeptides, the polynucleotides, antibodies and compositions of the  
 CC invention can be used as vaccines, as diagnostic reagents, and as  
 CC immunogenic compositions. The polypeptides can be used in the manufacture  
 CC of medicaments for treating or preventing infection due to *Neisseria*  
 CC bacteria (e.g. meningitis and septicemia), to detect the presence of  
 CC *Neisseria* bacteria, or to raise antibodies. They may also be used to  
 CC screen for agonists or antagonists, which may themselves have use as  
 CC antibacterial agents. The polynucleotides of the invention may also be  
 CC used in gene therapy protocols  
 XX Sequence 272 AA;  
 SQ

Query Match 22.9%; Score 297; DB 3; Length 272;  
 Best Local Similarity 31.8%; Pred. No. 3.5e-20;  
 Matches 84; Conservative 42; Mismatches 124; Indels 14; Gaps 6;

QY 1 MNRNRLVATVALSASCDVRSKDKQDQGSILVEYKDNKDTNDIELSDNQLSRFTFG 60  
 DB 1 MNTFKISALTLSAALSACGKKEAPASASEPAAASAQDTSIG-STWQQASYANG 59

QY 61 HLLARQLR--KSEDFFDIAEVAKGLQAEVLVCKSAPLTETEEYK--AEVQKLVPFK 114  
 DB 60 VDGRSLQKMEQGAIEDLVKFTQEAQVYDQKEIKMTEEQAEVMMKFLQEQAKAVEK 119

QY 115 ---KSKENLSLAELKFKNSKNAGVVEQPSKLYKIIKEGAGKAIKSPSALLHYKGSF 171  
 DB 120 HKADAKANKKEGAFLKNAADKG-VKTTASGLQYKITQKGEGKQPTKDDIVTVEYEGRL 178

QY 172 INGQVFSSEGNNEPILLPLGQTFPGALGMQKGEKTRVLVIHPDLAY---GTAGQLP 228  
 DB 179 IDGTVFDSKANGGPFVTFPLSQVIFGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIG 238

QY 229 PNSLLIFEINLIQASADEVAAPVQ 252  
 DB 239 PNATLVFDVKLVKIGAPENAPAKQ 262

RESULT 11  
 ID AAB25632 standard; protein; 272 AA.  
 XX AAB25632;  
 AC AAB25632;  
 XX 04-DEC-2000 (first entry)  
 XX N. meningitidis amino acid sequence m576-1.pep SEQ ID NO:987.  
 XX *Neisseria meningitidis*; *Neisseria gonorrhoeae*; genome; immunogenic;  
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;  
 KW *Meningococcus B*; MenB.  
 XX *Neisseria meningitidis*.  
 OS *Neisseria meningitidis*.  
 XX WO200022430-A2.  
 PN 20-APR-2000.  
 XX 08-OCT-1999; 99WO-US023573.  
 XX 09-OCT-1998; 98US-0103794P.  
 PR 30-APR-1999; 99US-0132068P.  
 XX (CHIR ) CHIRON CORP.  
 PA Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;  
 PI Massignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;  
 PI Rappuoli R, Pizza M;  
 XX WPI; 2000-318079/27.

DR N-PSDB; AAA81272.  
 XX Isolated nucleotide sequences of *Neisseria meningitidis* which can be used  
 PT in the diagnosis and treatment of *N. meningitidis* infection and other  
 PT *Neisseria* infections, for example, *N. gonorrhoea*.  
 XX Claim 14; Page 78; 1760pp; English.  
 XX The present invention describes methods of obtaining immunogenic proteins  
 CC from *Neisseria* genomic sequences. AAA81453 to AAA82414 represent  
 CC specifically claimed *Neisseria meningitidis* genomic DNA sequences;  
 CC AA81860 to AA81303 and AAB25620 to AAB25663 represent *Neisseria* DNA  
 CC sequences and their corresponding proteins; AAA81254 to AAA81259 and  
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of  
 CC *Neisseria meningitidis* DNA sequences; and AAA81322 to AAA81452 represent  
 CC *Neisseria meningitidis* MenB polynucleotide ORF sequences, which are all  
 CC used in the exemplification of the present invention. The nucleic acid  
 CC sequences, protein sequences, and antibodies against them, can be used in  
 CC the manufacture of a composition. The composition can be used as a  
 CC medicament (or in the manufacture of a medicament) for treating,  
 CC preventing or diagnosing infection due to *Neisseria* bacteria. For  
 CC example, some of the identified proteins could be components of vaccines  
 CC against *Meningococcus B*; against all serotypes; and/or against all  
 CC pathogenic *Neisseriae*. Identification of sequences from the bacterium  
 CC will also facilitate production of biological probes, particularly  
 CC organism-specific probes. Attempts to make efficacious *Meningococcus B*  
 CC vaccines have failed mainly due to antigen tolerance. Multivalent  
 CC vaccines have also been tried but none have successfully overcome  
 CC antigenic variability. The provision of further, complete sequences may  
 CC provide an opportunity to identify secreted or surface exposed proteins  
 CC that may be presumed targets for the immune system and which are not  
 CC antigenically variable or at least more conserved than other more  
 CC variable regions  
 XX Sequence 272 AA;  
 SQ

Query Match 22.9%; Score 297; DB 3; Length 272;  
 Best Local Similarity 31.8%; Pred. No. 3.5e-20;  
 Matches 84; Conservative 42; Mismatches 124; Indels 14; Gaps 6;

QY 1 MNRNRLVATVALSASCDVRSKDKQDQGSILVEYKDNKDTNDIELSDNQLSRFTFG 60  
 DB 1 MNTFKISALTLSAALSACGKKEAPASASEPAAASAQDTSIG-STWQQASYANG 59

QY 61 HLLARQLR--KSEDFFDIAEVAKGLQAEVLVCKSAPLTETEEYK--AEVQKLVPFK 114  
 DB 60 VDGRSLQKMEQGAIEDLVKFTQEAQVYDQKEIKMTEEQAEVMMKFLQEQAKAVEK 119

QY 115 ---KSKENLSLAELKFKNSKNAGVVEQPSKLYKIIKEGAGKAIKSPSALLHYKGSF 171  
 DB 120 HKADAKANKKEGAFLKNAADKG-VKTTASGLQYKITQKGEGKQPTKDDIVTVEYEGRL 178

QY 172 INGQVFSSEGNNEPILLPLGQTFPGALGMQKGEKTRVLVIHPDLAY---GTAGQLP 228  
 DB 179 IDGTVFDSKANGGPFVTFPLSQVIFGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIG 238

QY 229 PNSLLIFEINLIQASADEVAAPVQ 252  
 DB 239 PNATLVFDVKLVKIGAPENAPAKQ 262

RESULT 12  
 AAB58562  
 ID AAB58562 standard; protein; 272 AA.  
 XX AAB58562;  
 AC AAB58562;  
 XX 13-MAR-2001 (first entry)  
 XX N. meningitidis amino acid sequence m576-1.pep SEQ ID NO:27.  
 DE *Neisseria meningitidis*; *Neisseria gonorrhoeae*; immunogenic; vaccine;  
 XX diagnosis; antigen; detection; infection; gene therapy; antibacterial.  
 KW



Db 1 MNTFKISALTLTSLAALALSCGKKKEAAPASASBPAAASSAQGGDTSSIG--STMQQAASYANG 59

QY 61 HLLARQLR--KSEDMFFDIAEAVAKGLQAEVLCKVSAPLTETYEBEKM----AEVQKLKLVFEK 114

Db 60 VDIGHSLKQMKEQGAIEDLKVFTEAMQAVVDGKEIKWTEBQAQGVMMKFLQEQQAKAVEK 119

QY 115 ---KSKENLSLAEKPLKENSKNAGVBEVQPSKIQYKIIKEGAKAISGKPSALLHYKGSF 171

Db 120 HKADAKANKKEGAFLKENAADKG-VKTTASGLQYKITKQEGCKPTKDDIVTVEYEGRL 178

QY 172 INGVQVFSSEGNBPILLPLGCTIPGFALGCMQMKGEETRVLYIHPDLAY---GTAGQLP 228

Db 179 IDGTVFDSKANGGVFTPLPSQVLTGWTEGVQLLKEGGEATFYPSNLAYREQAGDKTG 238

QY 229 PNSLLIFEINLIQASADEVAAPVQ 252

Db 239 PNATLVFDVKLVKIGAPENAPAKQ 262

RESULT 15

ID AAY75137

ID AAY75137 standard; protein; 272 AA.

AC AAY75137;

XX

XX 21-MAR-2000 (first entry)

XX

DE Neisseria meningitidis ORF 576 protein sequence SEQ ID NO:1748.

XX

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;

KW antibacterial; gene therapy.

XX

OS Neisseria meningitidis.

XX

XX WO957280-A2.

PN

XX

PD 11-NOV-1999.

PD

PF 30-APR-1999; 99WO-US009346.

PF

XX 01-MAY-1998; 98US-0083758P.

XX

PR 31-JUL-1998; 98US-0094869P.

PR

PR 02-SEP-1998; 98US-0098994P.

PR

PR 02-SEP-1998; 98US-0099062P.

PR

PR 09-OCT-1998; 98US-0103749P.

PR

PR 09-OCT-1998; 98US-0103794P.

PR

PR 09-OCT-1998; 98US-0103796P.

PR

PR 25-FEB-1999; 99US-0121528P.

XX

PA (CHIR ) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.

XX

PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;

PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;

PI Tettelin H, Venter JC;

XX

DR WPI: 2000-062150/05.

DR N-PSDB; AA253899.

DR

XX

PT Novel Neisserial polypeptides predicted to be useful antigens for

PT vaccines and diagnostics.

XX

XX Claim 2; Page 893; 1453pp; English.

XX

CC AA253015 to AA254536, AA254577 to AA254615, and AA274253 to AA275941

CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides

CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent

CC PCR primers used in the exemplification of the present invention. The

CC polypeptides, the polynucleotides, antibodies and compositions of the

CC invention can be used as vaccines, as diagnostic reagents, and as

CC immunogenic compositions. The polypeptides can be used in the manufacture

CC of medicaments for treating or preventing infection due to Neisserial



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 12:10:53 ; Search time 39 Seconds  
(without alignments)  
438.719 Million cell updates/sec

Title: US-10-022-832-2

Perfect score: 1299

Sequence: 1 MNRRLNLVLTATLALSAS.....LIQASADEVAAPQEGNQGE 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1299	100.0	258	4	US-09-198-452A-699
2	305.5	23.5	249	4	US-09-328-352-5608
3	287.5	22.1	269	4	US-09-762-878-4
4	282.5	21.7	269	4	US-09-762-878-2
5	263	20.2	323	4	US-09-252-991A-17899
6	253	19.5	246	4	US-09-328-352-5613
7	237	18.2	254	4	US-09-489-039A-10914
8	233.5	18.0	255	4	US-09-543-681A-6784
9	226	17.4	239	4	US-09-809-665A-143
10	219	16.9	218	4	US-09-252-991A-21404
11	185.5	14.3	223	4	US-09-543-681A-5818
12	167.5	12.9	257	4	US-09-489-039A-8908
13	160	12.3	157	4	US-09-270-767-44323
14	159	12.2	107	3	US-08-894-173-69
15	159	12.2	107	3	US-08-894-173-83
16	159	12.2	107	3	US-09-398-193-69
17	159	12.2	107	3	US-09-398-193-83
18	159	12.2	119	5	PCT-US92-03993-1
19	159	12.2	120	1	US-08-336-618-17
20	156	12.0	412	2	US-08-741-134-2
21	150.5	11.6	230	4	US-09-481-620A-111
22	150	11.5	107	3	US-08-894-173-82
23	150	11.5	107	3	US-09-398-193-82
24	150	11.5	108	3	US-08-714-071-1
25	149.5	11.5	137	4	US-09-481-620A-85
26	149	11.5	107	1	US-08-197-795-2
27	149	11.5	107	1	US-08-336-618-15

28	149	11.5	107	5	PCT-US92-03993-3	Sequence 3, Appli
29	149	11.5	107	5	PCT-US95-01721-2	Sequence 2, Appli
30	148	11.4	103	1	US-08-197-795-1	Sequence 1, Appli
31	148	11.4	103	5	PCT-US95-01721-1	Sequence 1, Appli
32	146	11.2	108	2	US-08-803-899-4	Sequence 4, Appli
33	143	11.0	107	1	US-08-336-618-13	Sequence 13, Appli
34	143	11.0	107	2	US-08-963-601-1	Sequence 1, Appli
35	143	11.0	107	2	US-08-744-701-7	Sequence 7, Appli
36	143	11.0	107	3	US-08-894-173-67	Sequence 67, Appli
37	143	11.0	107	3	US-08-894-173-80	Sequence 80, Appli
38	143	11.0	107	3	US-09-398-193-67	Sequence 67, Appli
39	143	11.0	107	3	US-09-398-193-80	Sequence 80, Appli
40	143	11.0	107	4	US-08-735-848-1	Sequence 1, Appli
41	143	11.0	107	5	PCT-US92-03993-2	Sequence 2, Appli
42	143	11.0	108	1	US-07-822-966B-5	Sequence 5, Appli
43	143	11.0	108	2	US-08-803-899-3	Sequence 3, Appli
44	143	11.0	127	4	US-09-481-620A-40	Sequence 40, Appli
45	143	11.0	127	4	US-09-481-620A-72	Sequence 72, Appli

ALIGNMENTS

RESULT 1

US-09-198-452A-699  
; Sequence 699, Application US/09198452A  
; Patent No. 659294  
; GENERAL INFORMATION:  
; APPLICANT: Grifflais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198.452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 699  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-699

Query Match 100.0%; Score 1299; DB 4; Length 258;  
Best Local Similarity 100.0%; Pred. No. 6.3e-122;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNRRLNLVLTATLALSASCDVRSKDKDQGSILVEYKDKNDTNDIELSDNQLSRITFG	60
Db	1	MNRRLNLVLTATLALSASCDVRSKDKDQGSILVEYKDKNDTNDIELSDNQLSRITFG	60
Qy	61	HLLARQLRKSEDMFDDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVPEKKSKENL	120
Db	61	HLLARQLRKSEDMFDDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVPEKKSKENL	120
Qy	121	SLAEKFLKSNKAGVEVQPSKLYKIIEKGAGKATSGKPSALLHYKSGFINGQVFSSS	180
Db	121	SLAEKFLKSNKAGVEVQPSKLYKIIEKGAGKATSGKPSALLHYKSGFINGQVFSSS	180
Qy	181	EGNNEPILLPLGQITPGFALCMQMGKEGTRVLVTHPLAYGTAGQLPNSLLIIFEINLI	240
Db	181	EGNNEPILLPLGQITPGFALCMQMGKEGTRVLVTHPLAYGTAGQLPNSLLIIFEINLI	240
Qy	241	QASADEVAAPQEGNQGE	258
Db	241	QASADEVAAPQEGNQGE	258

RESULT 2

US-09-328-352-5608  
; Sequence 5608, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.

```

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5608
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5608

```

Query Match	23.5%	Score	305.5	DB 4	Length	249			
Best Local Similarity	32.7%	Pred. No.	2.1e-22						
Matches	82	Conservative	45	Mismatches	87	Indels	37	Gaps	7
Qy	3	RRNVLVLATVALALSV-ASCDVRGKDKDKDOGSLVYKDNKDTNDIELSDNKLKSLRTFGH	61						
Db	20	KKISLVIAASTMSLVFAAAPITNKPADQ-----FSYSGY	57						
Qy	62	LLARQLRKS-EDMFFDIAEVAKGLQAEVLCKSAPITETE-----YEEKMAEVLQKLVFE	113						
Db	58	LMGRNNTDALTDLNLDT--FYQGQGEQAQNKARTLDEEMAKAINDYKKTLEAKQLVFEFQ	115						
Qy	114	KSKENLSLAEKFLKENSKNAGVVEVOPSKLOYKIIKEGAGKAIKSGPSALLHYKGSFIN	173						
Db	116	KQGQQAQAAGAAFLAENAKKSGVVTK-SGLQYQVLKESGSKTPKATSRVKVNYEGRLD	174						
Qy	174	GOVFSSEGNEPILLPLGQTIPGALGMQMGKEGTRVLYIHDPDAYGTAG-----QLPPN	230						
Db	175	GTVPDSSIARNHPVDVQLNQVIAGTWEGTLQTMKSGGKTRFFIPAKLAYGEVGAGDSIGFN	234						
Qy	231	SLLIIFEINLIQ	241						
Db	235	STLIFDIELLO	245						

```

RESULT 3
US-09-762-878-4
; Sequence 4, Application US/09762878
; Patent No. 6706271
; GENERAL INFORMATION:
; APPLICANT: Thomard, Joelle
; TITLE OF INVENTION: Cloning of BASB023 Antigen from
; FILE REFERENCE: BM45329 Moraxella Catarrhalis
; CURRENT APPLICATION NUMBER: US/09/762,878
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: PCT/EP99/05828
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: GB 9817824.7
; PRIOR FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Bacteria
US-09-762-878-4

```

	Query Match	22.1%	Score 287.5;	DB 4;	Length 269;
	Best Local Similarity	32.7%;	Pred. No. 1.5e-20;		
	Matches	86;	Conservative 44;	Mismatches 100;	Indels 33; Gaps 10;
<hr/>					
QY	8	VLATVALALSVASCDVRSKDKDQGSLVEYKKNKTNDIELSN----	QKLSTFFGHLL	63	
Dd	:	: ::  :	:::	:::	:::
	6	LVATMAATLIVGC-----	QKDTSASLPKAGEKST---	VVSDDKSTEIEQSVMFYGDA	55
<hr/>					
QY	64	AROLRKSDMFDFIAEVAK-----	GLOAELVCKSAPLTETEEVKMAB--	VOKLVFEK	114
Dd	:	: ::  :	:::	:::	:::
<hr/>					
Dd	56	GESMKKLEEN-LDIIDVIKAFPGGYAGVDLSALTKKQTQLGQAIVEKRTTEEAIRQO--	QQ	112	
<hr/>					
QY	115	KSKENTSLAEKFUKENSNGAVGWEPQPSKLYKIIKEGACGRAISGGPKSALLHYGSFGING		174	

[illegible]

RESULT 4  
US-09-762-878-2  
Sequence 2, Application US/09762878  
Patent No. 6706271  
GENERAL INFORMATION:  
APPLICANT: Thonnard, Joelle  
TITLE OF INVENTION: Cloning of BASB023 Antigen from  
MORAXELLA CATARRHALIS  
FILE REFERENCE: BM45329  
CURRENT APPLICATION NUMBER: US/09/762.878  
CURRENT FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: PCT/EP99/05828  
PRIOR FILING DATE: 1999-08-11  
PRIOR APPLICATION NUMBER: GB 9817824.7  
PRIOR FILING DATE: 1998-08-14  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 269  
TYPE: PRT  
ORGANISM: Bacteria  
US-09-762-878-2

Query Match	21.7%	Score	282.5	DB	4	Length	269;
Best Local Similarity	32.3%	Pred. No.	4.7e-20;				
Matches	85;	Conservative	44;	Mismatches	101;	Indels	33;
Gaps	10						
Qy	8	VLATVALALSVASCDVRSKDKDQGSLVEYKONKDNDIELSON----	QKLSRTFGHLL	63			
		: ::  :	::  :	:	:	:	:
Db	6	LVIATMAATLILVGC-----	QKDTASLPKAGEKST--	VVSDKSTEIEQVSYYVGDA	55		
		: ::  :	::  :	:	:	:	:
Qy	64	ARQLRKSEDMFFDIAEVAK-----	GLQELVCKSAPLTETETEVEEKAAE--	VQKLVEEK	114		
		: ::  :	::  :	:	:	:	:
Db	56	GESMKKLEEN-LDIIDVVYIKAFKGAGVDSALTQQIQTGLQAAYEKKTETEEAIQK--	QQ	112			
		: ::  :	::  :	:	:	:	:
Qy	115	KSKENLSLABKFUKENSKNAGVVEVPQSFKQYKIIEKGACGAKAISGKPFSALLHYKGSFING	174				
		: ::  :	::  :	:	:	:	:
Db	113	AAVTNKADGEKFLAENAKDG-VKTTTPPGLOQYKVITEGTSKPSATAKDGVYAAYEGRLIDG	171				
		: ::  :	::  :	:	:	:	:
Qy	175	QVFSSSGNNNEPILLPIGOTIPGFALCMOGMKEGETRVLYTHPDLAYCTAQ-----	LPNN	230			
		: ::  :	::  :	:	:	:	:
Db	172	TVFDSSSGEAIVPFM--USQVTEGMSEGQLMKGGKYELYVPSQMAYGEHGMYNAGIGPN	229				
		: ::  :	::  :	:	:	:	:
Qy	231	SLLIFEINLIQASADEVAAPQE	253				
		: ::  :	::  :	:	:	:	:
Db	230	SVLVFVIDLKKSDEKAIAAEQQ	252				
		: ::  :	::  :	:	:	:	:

RESULT 5  
US-09-252-991A-17899  
; Sequence 17899, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18

```

: PRIOR APPLICATION NUMBER: US 60/094,130
:
: PRIOR FILING DATE: 1998-07-27
:
: NUMBER OF SEQ ID NOS: 3142
:
: SEQ ID NO 17899
:
: LENGTH: 323
:
: TYPE: prt
:
: ORGANISM: pseudomonas aeruginosa
US-09-252-991A-17899

```

Query Match	20.2%;	Score 263;	DB 4;	Length 323;
Best Local Similarity	31.6%;	Pred. NO. 5.6e-18;		
Matches	77;	Conservative 36;	Mismatches 105;	Indels 26; Gaps 5;

[illegible]

Qy 63 LARQLRKSEDMFFDIAEVAQGLQBLVCKSAPLTETETEEKMAEVOQLVPEKKS-----KEN 119

Dh 113 MGKSL-SOEGMDDLLSKAVAGKIGTINLKKYKQOVLTTSEELTFATAFYTKCPAEEDMAATGDEN 172

QY 120 LSLAEKFLKENSAGVVEQPSKLYKIIKEGAKAISGKPSALLHYKGSFINGOVFSS 179

DB 172 ASVCKEYKFLNCKDCKLCTM TTTACGLQVATYKYSQQGQDQKMTATYKTYKMTAT 221

Q7 180 SEGNNPIILPLGOTIPGFALGMQMKEGEITRVLYIHPDIAYGT---AQQLPPNSLLIFE 236

Qy 237 INLI 240  
: | :

## RESULT 6

```

US-09-328-352-5613
; Sequence 5613, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5613
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5613

```

Query Match	19.5%	Score 253;	DB 4;	Length 246;
Best Local Similarity	33.0%	Pred. No. 3.7e-17;		
Matches	68;	Conservative	33;	Mismatches 89;
				Indels 16;
				Gaps 4;

Qy	46	DIELSDNQKLSRTFGHLLARQLRKSDEDMFFEDIAEVAKGLQAEVLCKSAPLTETETEYEEKMA	105
Dh	43	DKVASPTQIKSYIVGVEVAQCTDPR---IDTKAFVQGIHDAARNKQPSAVTCEDIKAAVA	98

Qy 106 EVQKLVFEKXSKENL-----SLAEKFLKENSKNAGVVEVQPSKLOVKYIKEGAGKA 156

Dh 99 AVEVELOOCHOMCHOBEOBCTATMSADAOELAEKTKAG-VKTTTASCIQVLTITKCTCKO 157

QY 157 ISGKPSALHYKGSFINGOVFSSSGNNEPILLPGQTIPGFALGMQGMKEGETRVLVYIH 216

Qy 217 PDLAYG--TAGQLPNSLLIFEINLI 240  
: ||| : ||| : ||| : ||| : |||

RESULT 7  
 US-09-489-039A-10914  
 ; Sequence 10914, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary Breton et. al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 2709.2004001  
 ; CURRENT APPLICATION NUMBER: US/09/489,039A  
 ; CURRENT FILING DATE: 2000-01-27  
 ; PRIOR APPLICATION NUMBER: US 60/117,747  
 ; PRIOR FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 14342  
 ; SEQ ID NO 10914  
 ; LENGTH: 254  
 ; TYPE: PRT  
 ; ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-10914

Query Match	18.2%	Score 237;	DB 4;	Length 254;
Best Local Similarity	31.3%	Pred. No. 1.6e-15;		
Matches 68:	Conservative	40:	Mismatches 87:	Indels 22:
				Gaps 7

55 LSRFTGHLLARQLRKSDM--FFDIAEAVAKGLQAEVLCKSAPLTEYEE-----K 103

QY 104 MAEVOKLVFEKKSKENTSLAEKFLKENSAGVYVQPSKLOYKTIKEGAGKAISGPSPA 163

Q7 164 LLHYKGSFINGVFFSSSEGNNEPILLPLCQTIPGFALGMQMKGETRVLVIHPDLAYGT 223

QY 224 AG--QLPPNSLLIFEINLIQASADEVAAPQEGNQGE 258

```

RESULT 8
US-09-543-681A-6784
; Sequence 6784, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID S
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6784
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6784

```

Query Match	18.0%;	Score 233.5;	DB 4;	Length 255;
Best Local Similarity	27.9%;	Pred. No. 3.6e-15;		
Matches 70: Conservative	47;	Mismatches 113;	Indels 21;	Gaps 6

QY 7 LVLIATVALALSVASCDVRSKDKKDGQSILVEYKDNKOTNDIELSONQKLSTFGHLLAR 66

DH 15 LIATSIAAEFSADUALAERTAKVTINSAPKTONEFA-----VAICASMGDPWEAA 66

67 L--RKSEDMFFDIAEVAKGLQ-----AELVCKGAPLTETEYEEKGAEOVKLVFEKKSKE 118

QY 119 NLSLAELFKLNSKNAGVVEQPSKLYKIIEGAGKATSGKPSALLHYKGSFINGOVFS 178  
Db 127 NKAAGDKFTEFAAEKGVVVKTK-SGLLYLVENPGKKTPTDADRVTVNTKGMIDKQPD 185  
QY 179 SSEGNNPILLPLGQTIPGFALGMQMKGETRVLVIHPDLAYG---TAGQLPPNLSLLIF 235  
Db 186 SSVDRKEPLTISLKSVPQWTEGMKYIEGGKILVIPPPELGGQRATSG-IPANSTLVF 244  
QY 236 EINLIQASADE 246  
Db 245 EVELLSVESDK 255

RESULT 9

US-09-809-665A-143  
; Sequence 143, Application US/09809665A  
; Patent No. 6790950  
; GENERAL INFORMATION:  
; APPLICANT: Lowery E., David, et al.  
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions  
; FILE REFERENCE: 28341/00435 US/09/809,665A  
; CURRENT APPLICATION NUMBER: US/09/809,665A  
; PRIOR FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 60/153,453  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/128,689  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 09/545,199  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 143  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Actinobacillus pleuropneumoniae  
US-09-809-665A-143

Query Match 17.4%; Score 226; DB 4; Length 239;  
Best Local Similarity 29.3%; Pred. No. 1.8e-14;  
Matches 60; Conservative 43; Mismatches 86; Indels 16; Gaps 5;  
QY 56 SRTFGHLLARQLR-----KSEDMFFDIAEYAKGLQAEVLCKSAPLTETEYEEK----- 103  
Db 34 SYAVGLMGNIQGVESQKIEPSYQDKILAGVQ-DTIKTKGLTDEDLQKLSLDY 92  
QY 104 MAEYQKLVFEKSKENLSAEKFLKNSKNAGVVEQPSKLYKIIEGAGKATSGKPSA 163  
Db 93 LASQESKIAAEKSKATVEAGNKPRTDYEQSGVKKT-ASGLLYKIEKAGTGESPKAEDIV 151  
QY 164 LLHYKGSFINGOVFSSEGNNEPILLPLGQTIPGFALGMQMKGETRVLVIHPDLAYG- 222  
Db 152 KVHYKGLTDTGTVFSDSSYDRGEPIEFQLNQLIFGWIETPMLKKGKWEIVVPPPELGYGE 211  
QY 223 -TAGQLPPNLSLLIFEINLIQASADE 246  
Db 212 ROAGKIPASSTLKFEIELLDFAAE 236

RESULT 10

US-09-252-991A-21404  
; Sequence 21404, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 21404  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21404  
Query Match 16.9%; Score 219; DB 4; Length 218;  
Best Local Similarity 28.2%; Pred. No. 8e-14;  
Matches 57; Conservative 44; Mismatches 85; Indels 16; Gaps 5;  
QY 50 SDNQKLSRTFGHLLARQLRS-----EDMFFDIAEYAKGLQAEVLCKSAPLTETEYEE 102  
Db 21 TDEARVSYGIGKQLGDLQRENVPQMTLDAVLGSLDAFAGIDSRVSGEALSASFQVIRE 80  
QY 103 KM-AEVQKLVFEKSKENLSAEKFLKNSKNAGVVEQPSKLYKIIEGAGKATSGKPS 161  
Db 81 RMOAEAQ-----AKAEAAAGREGRAYLAENAKREGVT-VLPSTGLOFEVLSTGEGAKPSRED 134  
QY 162 SALLHYKGSFINGOVFSSEGNNEPILLPLGQTIPGFALGMQMKGETRVLVIHPDLAY 221  
Db 135 TVRTHYHGTLDGTVFSDSSYQYQGPAPFPVGVIAGWVEALQLMNAGSKWRLHVPSELAY 194  
QY 222 G--TAGQLPPNLSLLIFEINLIQ 241  
Db 195 GGOAVGSIPIPHSVLFDVELLE 216

RESULT 11

US-09-543-681A-5818  
; Sequence 5818, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 5818  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-5818

Query Match 14.3%; Score 185.5; DB 4; Length 223;  
Best Local Similarity 31.2%; Pred. No. 1.9e-10;  
Matches 62; Conservative 29; Mismatches 99; Indels 9; Gaps 5;  
QY 50 SDNQKLSRTFGHLLARQLRSSEDMFFDIAEYAKGLQAEVL--CKSAPLTETEYE--EKMA 105  
Db 25 STESQASYGIGLVQVQQLTESGLQGLEPAALLAGLTDALGNTPSVPV-ETLHNLRTWH 83  
QY 106 EVQKLVFEKSKENLSAEKFLKNSKNAGVVEQPSKLYKIIEGAGKATSGKPSALL 165  
Db 84 ERAEAVRQERQAALAEAGKVFLAENVKKEG-VQVTESGLQYKVLKAGDGAIPARTDHRV 142  
QY 166 HYKGSFINGOVFSSEGNNEPILLPLGQTIPGFALGMQMKGETRVLVIHPDLAYGTAG 225  
Db 143 HYTGRLIDGTVFSDSSVQYQGPAPFPVGVIAGWIEALTLMPVSGKWEIYIPQLAYGERG 202  
QY 226 ---QLPPNLSLLIFEINLIQ 241  
Db 203 AGAAIPFPFATLVFEVELLE 221

RESULT 12

US-09-489-039A-8908  
; Sequence 8908, Application US/09489039A  
; Patent No. 6610836



```

; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8908
; LENGTH: 257
; TYPE: prt
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8908

```

Query Match	12.9%; Score 167.5; DB 4; Length 257;
Best Local Similarity	27.7%; Pred. No. 1.5e-08;
Matches	53; Conservative 35; Mismatches 88; Indels 15; Gaps 4
QY	60 GHLIARQLRKS-----EDMFFDIAEAVAKGLQALVCKSAPLTETEEYEKMAEVQKLVF 112
Db	69 GLVQQQLSGLQCLIPALVAGIADALEGNQVPVEAVHRALETHERADAVRRERF 128
QY	113 EKSKENWLSAEKFLKENSKNAGVVEQPSKLOYKIIKEGAGKAISGPSALLHYKGSFI 172
Db	129 QAMAAD---GQKYLDENREKEGVNSTE-SGLQFRVLVTQGCPIPARTDRVRVHYTGKLI 183
QY	173 NGOVFSSESSEGNNEPILPLGQTIIPGFALGMOGMEGETRVLVIHPDLAYGTAG---QLPP 229
Db	184 DCTVFDSSVARGAEAPFVTGVIGWTEALTMLPVGSKWELTI PHNLAYGEGAGASIPP 243
QY	230 NSLLIFEINLI 240
Db	244 FSTLIFEVELL 254

```

RESULT 13
US-09-270-767-44323
; Sequence 44323, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44323
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44323

```

Query Match	12.3%	Score 160;	DB 4;	Length 157;
Best Local Similarity	29.4%	Pred. No. 3.9e-08;		
Matches	45;	Conservative	27;	Mismatches 63;
			Indels	18;
			Gaps	4
Qy	110	LVFEKKSKENLSLAETFLKENSKNAGVVEVPSKLOYKIIKEGACKAISGKPSALLHYKG	169	
Db	15	LAPDKMLTYILLICAFVAASADDPKV-----KIGIKKRVENCCTKAKGGDLVHVHYRG	69	
Qy	170	SFINGQVFSSEGNNEPTLLPLG--QTIPGPFALGMQGMKEGETRVLYITHPOLAYGTA---	224	
Db	70	ALQDGTETDSSYSRGTFPSFTLGARQVYKGDQGITLGMCEGEQRKLTTPPELGYCASGAG	129	
Qy	225	GQLPPNSLLIFEINLIQASADEVAAPQEQNQ	256	
Db	130	GKKIPPNVAVFDTELVKIE-----PRSGSE	155	

RESULT 14

```

US-08-894-173-69
; Sequence 69, Application US/08894173A
; Patent No. 6090612
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P14716C
; CURRENT APPLICATION NUMBER: US/08/894,173A
; CURRENT FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Neurospora crassa
; US-08-894-173-69

```

	Query Match	12.2%	Score 159;	DB 3;	Length 107;
	Best Local Similarity	39.8%;	Pred. No. 2.8e-08;		
	Matches	41;	Conservative 16;	Mismatches 40;	Indels 6; Gaps 3
Qy	144	LQYKIIKEGAGKAISGKPSAL-LHYKGSFINGVQFSSEGNNPEILLPL--GQTIPGPAL	200		
		: :   :	: :     :	:	:
Db	2	LQIEVQEGCGTRETRRGDNDVHYKGLTVSGKKFDASYDRGEPLNFVGQGVIKGWDE	61		
		: :   :	: :     :	:	:
Qy	201	GMOQMKGGETRVLYIHDPDLAG----TAGQLPPNSLLIFEINLI	240		
		: :     :	:	:	:
Db	62	GLLGMKIIGKRRLTIAPLAYGNRAVGGIIPANSTLIFETELV	104		
		: :     :	:	:	:

RESULT 15  
 US-08-894-173-83  
 ; Sequence 83, Application US/08894173A  
 ; Patent No. 6090612  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Medical Research Council  
 ; TITLE OF INVENTION: Adenylate cyclase and uses therefor  
 ; FILE REFERENCE: P14716C  
 ; CURRENT APPLICATION NUMBER: US/08/894,173A  
 ; CURRENT FILING DATE: 1997-08-13  
 ; NUMBER OF SEQ ID NOS: 97  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 83  
 ; LENGTH: 107  
 ; TYPE: PRT  
 ; ORGANISM: Neurospora crassa  
 ; US-08-894-173-83

[illegible]

Search completed: November 23, 2004, 12:11:41  
Job time : 40 secs

This page Blank (uspbid)

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 12:10:54 ; Search time 191 Seconds  
(without alignments)  
777.208 Million cell updates/sec

Title: US-10-022-832-2

Perfect score: 1299

Sequence: 1 MNRNRNVLATVALALSVAS.....LIQASAEVAAPQEGNQGE 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1299	100.0	258	1	MIP_CHLPN	Q927p3 chlamydia p
2	940	72.4	255	2	Q824R2	Q824x2 chlamydophi
3	934	71.9	255	2	Q46176	Q46176 chlamydophi
4	763	58.7	243	1	MIP_CHLTR	P26623 chlamydia t
5	733	56.4	243	1	MIP_CHLMU	Q9pjk1 chlamydia m
6	491.5	37.8	290	2	Q6WE92	Q6WE92 parachlamyd
7	491.5	37.8	290	2	CA23107	CA23107 parachlam
8	306	23.6	241	2	Q32827	Q32827 legionella
9	303.5	23.4	233	2	Q32836	Q32836 legionella
10	301	23.2	229	2	Q32821	Q32821 legionella
11	297	22.9	272	2	Q87YI8	Q9jy18 neisseria m
12	295.5	22.7	204	2	Q68494	Q68494 legionella
13	295.5	22.7	242	2	Q32767	Q32767 legionella
14	295	22.7	251	2	Q32768	Q32768 legionella
15	292.5	22.5	233	2	Q32749	Q32749 legionella
16	292.5	22.5	234	2	Q32844	Q32844 legionella
17	288.5	22.2	232	2	Q32763	Q32763 fluoribacte
18	288.5	22.2	233	2	Q32750	Q32750 legionella
19	288	22.2	232	2	Q6FFW0	Q6ffw0 acinetobact
20	287.5	22.1	233	2	Q32843	Q32843 legionella
21	287.5	22.1	234	2	Q32746	Q32746 legionella
22	287	22.1	235	2	Q6PFV9	Q6pfv9 acinetobact
23	287	22.1	272	2	Q87YJ0	Q9itj0 neisseria m
24	286	22.0	249	2	Q32751	Q32751 legionella
25	284	21.9	243	2	Q79DM1	Q79dm1 legionella
26	284	21.9	249	2	Q32766	Q32766 legionella
27	284	21.9	249	2	Q32820	Q32820 legionella
28	283.5	21.8	233	2	Q79863	Q79b63 legionella
29	283.5	21.8	257	2	Q87YB1	Q87yb1 pseudomonas
30	282.5	21.7	232	2	Q32842	Q32842 legionella
31	282.5	21.7	233	2	Q32839	Q32839 legionella

32	282	21.7	237	2	Q32762	Q32762 legionella
33	281.5	21.7	233	2	Q32838	Q32838 legionella
34	281	21.6	233	2	Q32835	Q32835 legionella
35	281	21.6	234	2	Q32759	Q32759 fluoribacte
36	281	21.6	241	2	Q32761	Q32761 legionella
37	280.5	21.5	234	2	Q32828	Q32828 legionella
38	279.5	21.5	233	2	Q32834	Q32834 legionella
39	279.5	21.5	234	2	Q32840	Q32840 legionella
40	279	21.5	238	2	Q7UKI6	Q7uk16 rhodospirill
41	279	21.5	243	1	MIP_LEGMI	P31106 legionella
42	279	21.5	244	2	Q32825	Q32825 tatlockia m
43	278.5	21.4	233	2	Q32752	Q32752 legionella
44	278	21.4	232	2	Q32747	Q32747 legionella
45	278	21.4	233	2	Q32826	Q32826 legionella

#### ALIGNMENTS

RESULT 1  
MIP\_CHLPN  
ID MIP\_CHLPN STANDARD; PRT; 258 AA.  
AC Q927P3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Peptidyl-prolyl cis-trans isomerase Mip precursor (EC 5.2.1.8)  
DE (PPIase) (Rotamase).  
GN Name=mip; OrderedLocusNames=CP00661, CP0086, CP00687;  
OS Chlamydia pneumoniae (Chlamydophila pneumoniae)  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.  
OX NCBI\_TaxID=83558;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CWL029;  
RX MEDLINE=99206606; PubMed=10192388; DOI=10.1038/77116;  
RA Kalman S., Mitchell W.P., Marathe R., Lammel C.J., Fan J., Hyman R.W.,  
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;  
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";  
RL Nat. Genet. 21:385-389(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR39;  
RX MEDLINE=20150255; PubMed=10684935;  
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
RA White O., Hickey E.K., Peterson J.D., Uterback T.R., Betsy K.J.,  
RA Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,  
RA Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,  
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;  
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";  
RL Nucleic Acids Res. 28:1397-1406(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=J138;  
RX MEDLINE=20330349; PubMed=10871362;  
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;  
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";  
RL Nucleic Acids Res. 28:2311-2314(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TW-183;  
RA Geng M.M., Schummacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,  
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;  
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: PPIases accelerate the folding of proteins.  
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline (omega=0).  
CC -!- SUBCELLULAR LOCATION: Outer membrane (By similarity).

```

CC -1- SIMILARITY: Belongs to the FKBP-type PPIase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; A5001648; AAD18800.1; -
DR EMBL; A5002172; AAF37972.1; -
DR EMBL; AP002547; BAA98868.1; -
DR EMBL; A5017159; AAP98616.1; -
DR PIR; B85573; B86573
DR PIR; F72052; F72052
DR HSSP; Q13451; 1KT0.
DR TIGR; CP0086; -
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS00059; FKBP_PPIASE_1.
DR PROSITE; PS00013; PROKAR LIPOPROTEIN; UNKNOWN 1.
KW Complete proteome; Isomerase; Outer membrane; Rotamase; Signal.
FT SIGNAL 1 15 Potential.
FT CHAIN 16 258 Peptidyl-prolyl cis-trans isomerase Mip.
FT DOMAIN 160 243 PPIase, FKBP-type.
SQ SEQUENCE 258 AA; 28330 MW; 65E3CE4EAC022552 CRC64;

Query Match 100.0%; Score 1299; DB 1; Length 258;
Best Local Similarity 100.0%; Pred. No. 4.9e-82;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRRLNLVLTALSVASCDVRSKDKQDQGSLSVEYKDKNDTNDIELSDNQKLSRTFG 60
Db 1 MNRRLNLVLTALSVASCDVRSKDKQDQGSLSVEYKDKNDTNDIELSDNQKLSRTFG 60
QY 61 HLLARQLRKSEDMFFDIAEVAKGLQELVCKAPLTETEYEKMAEVQKLVEPKSKENL 120
Db 61 HLLARQLRKSEDMFFDIAEVAKGLQELVCKAPLTETEYEKMAEVQKLVEPKSKENL 120
QY 121 SLAEKFLKSNKAGVVEVQPSKLYKIKEGAGKAIKSGKPSALLHYKGSFINGQVFSS 180
Db 121 SLAEKFLKSNKAGVVEVQPSKLYKIKEGAGKAIKSGKPSALLHYKGSFINGQVFSS 180
QY 181 EGNNEPILLPLGOTIPGFALGMQMKGEQTRVLYIHPDLAYGTAGQLPPNSLLIFEINLI 240
Db 181 EGNNEPILLPLGOTIPGFALGMQMKGEQTRVLYIHPDLAYGTAGQLPPNSLLIFEINLI 240
QY 241 QASADEVAAPQSGNOGE 258
Db 241 QASADEVAAPQSGNOGE 258

RESULT 2
Q824R2 PRELIMINARY; PRT; 255 AA.
ID Q824R2
AC Q824R2
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase Mip.
GN Name=mip; OrderedLocusNames=CCAA00078;
OS Chlamydomophila caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,

```

```

RA Heidelberg J.F., Holtzaple E.K., Khouri H.M., Federova N.B.,
RA Carty H.A., Unayam L.A., Haft D.H., Peterson J.D., Beanan M.J.,
RA White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G.,
RA Bavoil P.M., Fraser C.M.;
RT "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae";
RL Nucleic Acids Res. 31:2134-2147(2003).
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -1- SIMILARITY: Belongs to the FKBP-type PPIase family.
DR EMBL; A5016994; AAP04830.1; -
DR HSSP; P20380; 1FD9.
DR TIGR; CCA00078; -
DR GO; GO:001855; P:isomerase activity; IEA.
DR GO; GO:0008457; P:protein folding; IEA.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS00059; FKBP_PPIASE_3; 1.
KW Complete proteome; Isomerase; Rotamase.
SQ SEQUENCE 255 AA; 28195 MW; 84FD9C3E8EBB61DF CRC64;

Query Match 72.4%; Score 940; DB 2; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.5e-57;
Matches 181; Conservative 34; Mismatches 30; Indels 4; Gaps 1;

QY 1 MNRRLNLVLTALSVASCDVRSKDKQDQGSLSVEYKDKNDTNDIELSDNQKLSRTFG 60
Db 1 MNRRLNLVLTALSVASCDVRSKDKQDQGSLSVEYKDKNDTNDIELSDNQKLSRTFG 60
QY 61 HLLARQLRKSEDMFFDIAEVAKGLQELVCKAPLTETEYEKMAEVQKLVEPKSKENL 120
Db 61 HLLARQLRKSEDMFFDIAEVAKGLQELVCKAPLTETEYEKMAEVQKLVEPKSKENL 120
QY 121 SLAEKFLKSNKAGVVEVQPSKLYKIKEGAGKAIKSGKPSALLHYKGSFINGQVFSS 180
Db 121 SLAEKFLKSNKAGVVEVQPSKLYKIKEGAGKAIKSGKPSALLHYKGSFINGQVFSS 180
QY 181 EGNNEPILLPLGOTIPGFALGMQMKGEQTRVLYIHPDLAYGTAGQLPPNSLLIFEINLI 240
Db 181 EGNNEPILLPLGOTIPGFALGMQMKGEQTRVLYIHPDLAYGTAGQLPPNSLLIFEINLI 240
QY 241 QASADEVA 249
Db 241 QASADEVA 249
QY 237 ETTDDSVAA 245
Db 237 ETTDDSVAA 245

RESULT 3
Q46176 PRELIMINARY; PRT; 255 AA.
ID Q46176
AC Q46176
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mip protein.
GN Name=mip;
OS Chlamydomophila caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RX MEDLINE=97090413; PubMed=8936321;
RA Rockey D.D., Chesebro B.B., Heinzen R.A., Hackstadt T.;
RT "A 28 kDa major immunogen of Chlamydia psittaci shares identity with
RT Mip proteins of Legionella spp. and Chlamydia trachomatis-cloning and
RT characterization of the C. psittaci mip-like gene.";
RL Microbiology 142:945-953(1996).
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).

```

```

CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
DR EMBL; L39892; AAB41346.1; -.
DR HSP; F20380; IFD9.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS00059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 255 AA; 28271 MW; 8950F9F1E61961DF CRC64;

Query Match 71.9%; Score 934; DB 2; Length 255;
Best Local Similarity 72.3%; Pred. No. 9.2e-57;
Matches 180; Conservative 34; Mismatches 31; Indels 4; Gaps 1;

QY 1 MNRRLNLVATVALASVASCDSVRSKDKQGSILVEYKDKNTDNDIELSDNOKLSRTFG 60
DB 1 MKRWHLMIITVVSFSIASCDSQSGNQ-----IAQVEEKSANDSOLSVNQQLSRTFG 56

QY 61 HLLARQLRKSEDMFFDIAEAVAKGLQAEVLCKSAPLTETETEYBEKMAEVQKLVFEKKSKENL 120
DB 57 HLLARQLRKSEDMFFDIAEAVAKGLQAEVLCKSAPLTETETEYBEKMAEVQKLVFEKKSKENL 116

QY 121 SLAEKFLKSNKAGVVEQPSKLYKIIEGAGKAISGKPSALLHYKGSFINGQVFS 180
DB 117 YLAERFLOENKNSGVVEQADKLYRIYKSGTGRAISGKPSALLHYKGTIDGQVFS 176

QY 181 EGNNEPILLPGOTIPGALGQMGKEGTRVLYIHPDLAYCTAGOLPNSLLIFEINLI 240
DB 177 EANKPEILLPLAQTIPGALGQMGKEGTRILYIHPDLAYCTAGOLPNSLLIFEINLI 236

QY 241 QASADEVAA 249
DB 237 ETTDSVAA 245

RESULT 4
MIP_CHLTR
ID - MIP_CHLTR STANDARD; PRT; 243 AA.
AC P26623;
DT 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase Mip precursor (EC 5.2.1.8)
DE (PPIase) (Rotamase) (27 kDa membrane protein) (Chl-Mip).
GN Name=mip; OrderedLocustNames=CT541;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serovar B, Serovar E, and Serovar L2;
RX MEDLINE=93023883; PubMed=1406289;
RA Lundemose A.G., Rouch D.A., Birkelund S., Christiansen G.,
RT Pearce J.H.;
RA "Chlamydia trachomatis Mip-like protein.";
RL Mol. Microbiol. 6:2539-2548(1992).

[2]
RP SEQUENCE FROM N.A.
RC STRAIN=D/OW-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.I., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).

[3]
RN
RP SEQUENCE OF 69-243 FROM N.A.
RC STRAIN=Serovar L2;
RX MEDLINE=91194539; PubMed=2013997;

```

```

RA Lundemose A.G., Birkelund S., Fey S.J., Mose Larsen P.,
RA Christiansen G.;
RT "Chlamydia trachomatis contains a protein similar to the Legionella
RT pneumophila mip gene product.";
RL Mol. Microbiol. 5:109-115(1991).
CC -!- FUNCTION: PPIases accelerate the folding of proteins.
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X66126; CAA46917.1; -.
DR EMBL; X66127; CAA46918.1; -.
DR EMBL; X66128; CAA46919.1; -.
DR EMBL; AE001324; AAC68143.1; -.
DR PIR; S25255; S25255.
DR PIR; S28638; S28638.
DR HSP; P18203; 1FKL.
DR PHCI-2DPAGE; P26623; -.
DR Signa-2DPAGE; P26623; -.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS00059; FKBP_PPIASE; 1.
KW Complete proteome; Isomerase; Outer membrane; Rotamase; Signal.
FT SIGNAL 1 14
FT CHAIN 15 243
FT DOMAIN 152 235
FT VARIANT 56 56 S -> A (in serovar L2).
FT VARIANT 117 117 K -> E (in serovar L2).
FT CONFLICT 137 138 QY -> HD (in Ref. 3).
SQ SEQUENCE 243 AA; 26663 MW; 677F9D551A95A382 CRC64;

Query Match 58.7%; Score 763; DB 1; Length 243;
Best Local Similarity 61.1%; Pred. No. 6e-45;
Matches 149; Conservative 36; Mismatches 49; Indels 10; Gaps 2;

QY 5 WNLVLTVALASVASCDSVRSKDKQGSILVEYKDKNTDNDIELSDNOKLSRTFGHLLA 64
DB 7 WLMF---AVALPIVGC-----DNGGSGTSATEKSMVEDSALTDNOKLSRTFGHLLS 56

QY 65 RQLRKSEDMFFDIAEAVAKGLQAEVLCKSAPLTETETEYBEKMAEVQKLVFEKKSKENLSLAE 124
DB 57 RQLRTEDEFSLDLVEVYKMGQSEIDGQSAPLTETETEYBEKMAEVQKASFEAKCSENLSLAE 116

QY 125 KFLKSNKAGVVEQPSKLYKIIEGAGKAISGKPSALLHYKGSFINGQVFSSEGN 184
DB 117 KFLKENKEKAGVIELEPNKLYRVVKEGTGRVLSGKPTALLHYTGSFIDGKVFDSSEK 176

QY 185 EPILLPGOTIPGALGQMGKEGTRVLYIHPDLAYCTAGOLPNSLLIFEINLIQASA 244
DB 177 EPILLPLTKVIPGFSQGMQMGKEGEVRVLYIHPDLAYCTAGOLPNSLLIFEVKLIEND 236

QY 245 DEVA 248
DB 237 DNVS 240

RESULT 5
MIP_CHLMU
ID - MIP_CHLMU STANDARD; PRT; 243 AA.
AC Q9FUKI;
DT 16-OCT-2001 (Rel. 40, Created)

```

```

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 01-OCT-2004 (Rel. 45, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase Mip precursor (EC 5.2.1.8)
DE (PPIase) (Rotamase).
GN Name:mip; OrderedLocusNames=TC0828;
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mopn / Nigg;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Lincker E.K., Peterson J.D., Utterback T.R., Berry K.J.,
RA Bass S., Hickey K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA McDoson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
RA McClarty G., Salzman S.L., Eisen J.A., Fraser C.M.;
RA "genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -1- FUNCTION: PPIases accelerate the folding of proteins.
CC CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC CC -1- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC CC -1- SIMILARITY: Belongs to the FKBP-type PPIase family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/annouce/
CC or send an email to license@sib-sib.ch).
-----
DR EMBL; AE002349; AAF39628.1; ALT_INIT.
DR HSPG; P27124; IROT.
DR TIGR; TC0828; -.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS00059; FKBP_PPIASE; 1.
DR Complete proteome; Isomerase; Outer membrane; Rotamase; Signal.
KW SIGNAL
FT CHAIN
FT CHAIN 15 243 Peptidyl-prolyl cis-trans isomerase Mip.
FT DOMAIN 152 235 PPIase, FKBP-type.
FT DOMAIN 243 AA; 26781 MW; 4556004B7511A72C CRC64;
SQ SEQUENCE
Query Match 56.4%; Score 733; DB 1; Length 243;
Best Local Similarity 59.4%; Pred.No. 7.2e-43;
Matches 145; Conservative 35; Mismatches 54; Indels 10; Gaps 2;
QY 5 WNLVATVALALSVASCDVRSKDKDQGSVLVEYKDNKDNTNDIELSDNQKLRSRTFGHLLA 64
DB 7 WMLNF---AVALPLGC-----DNNGSQTSAMGDWEDSVLTNQKLRSRTFGHLLA 56
QY 65 RLQRKSEDMFDDIAEVAAGLQAEVLCKSAPIETETEYEKKMAEVQKLVPFKKSKEKNLSLA 124
DB 57 RLQSSTEDFTLDLFEVIKGMQSEIEGKSAPLTDSEYETQMALVQKASFEEKSCENLASAE 116
QY 125 KFLKENSKNAGVEVOPSKLOYKIIEKGANGKAISGKPSALLHYGSGTFINGOVFSSEGN 184
DB 117 KFLKENDKGEVILEPNKLGQYRIIVKEGTGRVLTGKPNALLHYTGSPFNGKVFDTSKNK 176
QY 185 EPILLPLGQTIPGPALMGQMKEGETRVLVYIHPDLAYGTACQLPPNSLLIPEINLIQASA 244
DB 177 DPILLPLTKVISGFSQGQGWREGEVRVLVYIHPDLAYGTSQQLPPNSLLIPEVKLEAND 236
QY 245 DEVA 248
DB :337 DNVS 240

```

[illegible]

RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,  
 RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,  
 RA Rattai T., Mewes H., Wagner M.;  
 RT "Genome sequence of an amoeba symbiont and its use for reconstructing  
 RT the evolutionary history of chlamydiae.";  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UW825;  
 RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,  
 RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,  
 RA Rattai T., Mewes H., Wagner M.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX908798; CAP23107.1; --  
 KW Isomerase.  
 SQ SEQUENCE 290 AA; 31682 MW; 1993E60549FE0B7E CRC64;

Query Match 37.8%; Score 491.5; DB 2; Length 290;  
 Best Local Similarity 49.0%; Pred. No. 4.7e-26;  
 Matches 96; Conservative 35; Mismatches 64; Indels 1; Gaps 1;

QY 51 DNQKLSRTFGHLLARQLRKSEDMFFDIAEVAQGLQAEVLVCKSAPILTETEYEKMAEVQKL 110  
 DB 51 DMQKLSAEAFGHFIGNL-QAPGLQFDLEAIKIGREGAAGKPAIPSEKEYEEMMAVQER 109  
 QY 111 VFEKSKENLSLAEKFLKSNAGVVEVQPSKLYKIIKEGAGKAIISGKPSALLHYKGS 170  
 DB 110 AFKEMSTKLNANDFMKNSQSTDTVEIPGKLYSVEKEGTGPVPEPHSPKIHVTKG 169  
 QY 171 FINGOVFSSSEGNNEPILLPGQTTPGALGMOGKEGTRVLYIHPDLAYGTAGOLPPN 230  
 DB 170 YQDGTVFSTSEMDGPIITPLDQTPGFSKGVGMKEGKRLRYVHPDLGYGTGQLPPN 229  
 QY 231 SLLEIFENLQASDE 246  
 DB 230 ELLIFDIEVRANSDD 245

RESULT 8  
 O32827 PRELIMINARY; PRT; 241 AA.  
 AC O32827;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Macrophage infectivity potentiator.  
 GN Name=mip;  
 OS Legionella nautarum.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
 OC Legionellaceae; Legionella.  
 OX NCBI\_TaxID=45070;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 49506;  
 RX MEDLINE=98010353; PubMed=9350870;  
 RA Ratcliff R.M., Donnellan S.C., Lanser J.A., Manning P.A.,  
 RA Heuzenroeder M.W.;  
 RT "Interspecies sequence differences in the Mip protein from the genus  
 RT Legionella; implications for function and evolutionary relatedness.";  
 RL Mol. Microbiol. 25:1149-1158(1997).  
 CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline  
 CC (omega=0).  
 CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.  
 DR EMBL; U22133; AAC45699.1; --  
 DR HSSP; P20380; 1FD9.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 RA Heuzenroeder M.W.;  
 RT "Interspecies sequence differences in the Mip protein from the genus  
 RT Legionella; implications for function and evolutionary relatedness.";  
 RL Mol. Microbiol. 25:1149-1158(1997).  
 CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline  
 CC (omega=0).  
 CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.  
 DR EMBL; U22133; AAC45699.1; --  
 DR HSSP; P20380; 1FD9.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR InterPro; IPR000774; FKBP\_Nterm.  
 DR InterPro; IPR001179; FKBP\_PPIase.  
 DR InterPro; IPR008104; INFPTNTIATR.  
 DR Pfam; PF00254; FKBP\_C; 1.  
 DR Pfam; PF01346; FKBP\_N; 1.  
 CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.  
 DR EMBL; U22133; AAC45699.1; --  
 DR HSSP; P20380; 1FD9.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR InterPro; IPR000774; FKBP\_Nterm.  
 DR InterPro; IPR001179; FKBP\_PPIase.  
 DR InterPro; IPR008104; INFPTNTIATR.  
 DR Pfam; PF00254; FKBP\_C; 1.  
 DR Pfam; PF01346; FKBP\_N; 1.

DR PRINTS; PR01730; INFPTNTIATR.  
 DR PRODOM; PD001516; FKBP\_Nterm; 1.  
 DR PROSITE; PS50059; FKBP\_PPIASE\_3; 1.  
 KW Isomerase; Rotamase.  
 SQ SEQUENCE 241 AA; 25788 MW; 2C36F75ABEAD9E93 CRC64;

Query Match 23.6%; Score 106; DB 2; Length 241;  
 Best Local Similarity 38.8%; Pred. No. 2.7e-13;  
 Matches 78; Conservative 31; Mismatches 80; Indels 12; Gaps 4;

QY 50 SDNQKLSRTFGHLLARQLRKSEDMFFDIAEVAQGLQAEVLVCKSAPILTETEYEKMAEVQK 109  
 DB 50 TDTDKLSYSICADLGKPKK-QGIDISPAAMAKGLQDCMSGQLLTTEQMKVNLKFKQK 94  
 QY 110 LV-----FEKSKENLSLAEKFLKSNAGVVEVQPSKLYKIIKEGAGKAIISGKPS 162  
 DB 95 ELMKRSAEFNKSKSEENKSGEAFKLNKSKDGVVSL-PSGLQVLYKILEKGDGAKPAKDDT 153  
 QY 163 ALLHYKGSFINGOVFSSSEGNNEPILLPGQTTPGALGMOGKEGTRVLYIHPDLAYG 222  
 DB 154 VTVEYTGRLINGQVDFDSTKTKPATFKVQSVIPGWTEALQMPGSGSTWVEVIPSCLAYG 213  
 QY 223 --TAGQLPPNSLLIFEINLI 240  
 DB 214 PRSVGGPIGNETLIFKHLI 234

RESULT 9  
 O32836 PRELIMINARY; PRT; 233 AA.  
 ID O32836  
 AC O32836;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Macrophage infectivity potentiator.  
 GN Name=mip;  
 OS Legionella quinlivanii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
 OC Legionellaceae; Legionella.  
 OX NCBI\_TaxID=45073;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 43830;  
 RX MEDLINE=98010353; PubMed=9350870;  
 RA Ratcliff R.M., Donnellan S.C., Lanser J.A., Manning P.A.,  
 RA Heuzenroeder M.W.;  
 RT "Interspecies sequence differences in the Mip protein from the genus  
 RT Legionella; implications for function and evolutionary relatedness.";  
 RL Mol. Microbiol. 25:1149-1158(1997).  
 CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline  
 CC (omega=0).  
 CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.  
 DR EMBL; U2217; AAC45703.1; --  
 DR HSSP; P20380; 1FD9.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.  
 DR GO; GO:0006457; P:protein folding; IEA.  
 DR InterPro; IPR000774; FKBP\_Nterm.  
 DR InterPro; IPR001179; FKBP\_PPIase.  
 DR InterPro; IPR008104; INFPTNTIATR.  
 DR Pfam; PF00254; FKBP\_C; 1.  
 DR Pfam; PF01346; FKBP\_N; 1.  
 DR PRINTS; PR01730; INFPTNTIATR.  
 DR PRODOM; PD001516; FKBP\_Nterm; 1.  
 DR PROSITE; PS50059; FKBP\_PPIASE\_3; 1.  
 KW Isomerase; Rotamase.  
 SQ SEQUENCE 233 AA; 24934 MW; 7F5E61B25249DC16 CRC64;

Query Match 23.4%; Score 303.5; DB 2; Length 233;  
 Best Local Similarity 33.9%; Pred. No. 3.8e-13;  
 Matches 85; Conservative 42; Mismatches 87; Indels 37; Gaps 7;

QY 10 ATVALALSVCDSVRSKDKDQGSLSVBYKONKOTNDIELS-DNQKLSRTFGHLLARQUR 68

	Query Match	23.2%	Score 301;	DB 2;	Length 229;	
	Best Local Similarity	37.0%;	Pred. No. 5.6e-13;			
	Matches	77;	Conservative 36;	Mismatches 81;	Indels 14;	Gaps 5;
<hr/>						
QY	50	SDNQLSRITGHLLAROL-RKSEDMFFDIAEVAKGLQAEVLCKCAPLITEYEERMAEVQ	108			
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
Dd	24	SDIDKLSYSGIDIGKNFKRQGIDVNPET--LVKGLQDGISGNKSLTTEDQMRLVDLKQF	81			
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
<hr/>						
QY	109	K-----LVFEKSKENLSLAELFKLENSKNAGVVEQPSKLOYKIKEGAGKAISKGP	161			
		: : : : :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
<hr/>						
Dd	82	KDLMAKRBTAYYQAAENKAKGEAFLENKAKEGWTL-PSGLQYKIIKSGSGKKPKGED	140			
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				

Query Match	22.9%	Score 297;	DB 2;	Length 272;
Best Local Similarity	31.8%;	Pred. No. 1.3e-12;		
Matches	84;	Conservative 42;	Mismatches 124;	Indels 14; Gaps 6;

  

QY	1	MNRRNLVLATVALALSASCDVRSKDKDQCSLVEYKDNTNDLELSDNOKLSRTFG	60
		: : :     : : :     : : :     : : :	
Db	1	MNTFIKISALTLSAALLSALSCGKEAPASAASEPAAAASSAGGTSSIG-STMQOASVAMG	59
		: : : : : : : : : : : : : : : : : : : : : :	
QY	61	HLLARQLR--KSBDMFDAEAVAKGLQAEVLCKSAPLTETETEYEKMG---AEVQKLVEFK	114
		: : : : : : : : : : : : : : : : : : : : : :	
Db	60	VDIRSLQKWQEGASIDILKVFTTEAQVVDGHEIKMTTEEQAQEVMMVKFLQEQQAKAVEK	119
		: : : : : : : : : : : : : : : : : : : : : :	
QY	115	----KSKENLSLAEBKFLENKSNAGVVVEOPSKLYKIIEKGAGKAISGKPSALLHYKGSF	171



```
Db 120 HKADAKANKKEGEAFLENAADKG-VKTTAGSLQYKTKQEGKQPTKDDIVTVEYEGRL 178
Qy 172 INGQVFSSEGNBPILLPLGQTTPGPFALGMQMGKEGTRVLYIHPDLAY---GTAGQLP 228
Db 179 IDGTVFSSKANGGVFPFLSQVPGTWEGVOLLKEGGEATFYPSNLAYREQGAGDKIG 238
Qy 229 PMSLIFINLIQASAEVAAPVQ 252
Db 239 ENATLVFDVKLVKIGAPENAPAKQ 262

RESULT 12
ID O68494 PRELIMINARY; PRT; 204 AA.
AC O68494;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Macrophage infectivity potentiator protein (Fragment).
GN Name=mip;
OS Legionella sp. L.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=74303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LC1863;
RX MEDLINE=98281687; PubMed=9620377;
RA Ratcliff R.M., Lanser J.A., Manning P.A., Heuzenroeder M.W.;
RT "Sequence-based classification scheme for the genus Legionella
targeting the mip gene.";
RL J. Clin. Microbiol. 36:1560-1567(1998).
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
(omega=0).
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
DR EMBL; AF047754; AAC08978.1; -.
DR HSSP; P20380; 1FD9.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF01346; FKBP_N; 1.
DR PRINTS; PR01730; INFPTNTIATR.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
FT NON_TER 1
FT NON_TER 204
SQ SEQUENCE 204 AA; 22279 MW; 4E87F5B3A2CF6889 CRC64;

Query Match 22.7%; Score 295.5; DB 2; Length 204;
Best Local Similarity 34.9%; Pred. No. 1.2e-12;
Matches 76; Conservative 34; Mismatches 77; Indels 31; Gaps 4;

Qy 12 VALALSVASCDVRKDKQGSILVEYKDKNDIELSDNQLSRRTFGHLLARQIRKSE 71
Db 7 LAMTTTAAATDQSLNKKD-----KLSYSTGIDIGKKNFRX-Q 43
Qy 72 DMFFDIAEVAKGLQAEVLCKSAPLTETEYEEKMAEVQKLVPEKKS 124
Db 44 GLEVNPVLAKGQGLSGSKQLLDEQNKVLSNFQKSLMAKRTAEFNKKAENKQKE 103
Qy 125 KFLKNSKNAGVVEQPSKLYKIIKEGAGKAISGKPSALLHYKGSFINGQVFSSEGN 184
Db 104 AFLKNSKKEGVVAL-PSGLQYKIIKEGAGKPKTEDVVTVEYTGRLINGDVFDSTKSG 162
Qy 185 EPILLPLGQTTPGPFALGMQMGKEGTRVLYIHPDLAYG 222
Db 163 KPATFKLSQVPGTWTEALQLMPEGSTWIIYVPSDLAYG 200
```

```
RESULT 13
ID O32767 PRELIMINARY; PRT; 242 AA.
AC O32767;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Macrophage infectivity potentiator.
GN Name=mip;
OS Legionella israelensis;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43119;
RX MEDLINE=98010353; PubMed=9350870;
RA Ratcliff R.M., Donnellan S.C., Lanser J.A., Manning P.A.,
Heuzenroeder M.W.;
RT "Interspecies sequence differences in the Mip protein from the genus
Legionella: implications for function and evolutionary relatedness.";
RL Mol. Microbiol. 25:1149-1158(1997).
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
(omega=0).
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
DR EMBL; U92208; AAC45692.1; -.
DR HSSP; P20380; 1FD9.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR008104; INFPTNTIATR.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR PRINTS; PR01730; INFPTNTIATR.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 242 AA; 26162 MW; 7B6ADF5B67ABBCD CRC64;

Query Match 22.7%; Score 295.5; DB 2; Length 242;
Best Local Similarity 31.6%; Pred. No. 1.4e-12;
Matches 80; Conservative 44; Mismatches 92; Indels 37; Gaps 6;

Qy 7 LVLATV---ALALSVASCDVRKDKQGSILVEYKDKNDIELSDNQLSRRTFGHLL 63
Db 5 LVAATVMSMAISTAATAATDASSLN-----TDVEKLSYSIGADL 42
Qy 64 ARQLRKSEDMFFDIAEVAKGLQAEVLCKSAPLTE-----TEYEEKMAEVQKLVPEKKS 116
Db 43 GKNFKK-QGIEDIDPQMAAGKMGDGLKLTQEQMDVLNKFQELMAKENAEFNKA 101
Qy 117 KENLSLAEKFLKNSKNAGVVEQPSKLYKIIKEGAGKAISGKPSALLHYKGSFINGQV 176
Db 102 AENKAKGEAFLEQNKKEGVVTL-PSGLQYKIIKEGAGKPKTEDVVTVEYTGRLINGQV 160
Qy 177 FSSSEGNNEPILLPLGQTTPGPFALGMQMGKEGTRVLYIHPDLAYG---TAQLPNSLL 233
Db 161 FDSSEVRGKPTAFKVSQVPGTWTEALQMLPAGSTWIIYVPSDLAYGPRISIGGPIGNETL 220
Qy 234 IFEINLIQASAE 246
Db 221 IFKHLIISVKDK 233

RESULT 14
ID O32768 PRELIMINARY; PRT; 251 AA.
AC O32768;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
```

```

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Macrophage infectivity potentiator.
GN Name=miip;
OS Legionella jordanis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=456;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33263;
RX MEDLINE=98010353; PubMed=9350870;
RA Ratcliff R.M., Donnellan S.C., Lanser J.A., Manning P.A.,
RA Heuzenroeder M.W.;
RT "Interspecies sequence differences in the Mip protein from the genus
RT Legionella; implications for function and evolutionary relatedness.";
RL Mol. Microbiol. 25:1149-1158 (1997).
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
DR EMBL; U91608; AAC45670.1; -
DR HSSP; P20380; 1FD9.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR008104; INFOTNTIATR.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR PRINTS; PR01730; INFOTNTIATR.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 251 AA; 26681 MW; EAE0386659994331 CRC64;

Query Match 22.7%; Score 295; DB 2; Length 251;
Best Local Similarity 33.5%; Pred. No. 1.6e-12;
Matches 86; Conservative 39; Mismatches 110; Indels 22; Gaps 7;

QY 4 RNVLVLTAV---ALALSVASCDVRSKDKDQGSILVEYKDKNDNDIEL-SDNKLSTRTF 59
DB 2 KMLRLVAAVGLAMTGAIAANDATNTATSPAS-----NTATSATSLNSDMDKLSYSI 55
QY 60 GHLLARQLRKSDFDIAEVAKQLAELVCKSAPLTETETEYEEKMAEVOK-----LVP 112
DB 56 GADLGRNFKK-QGIDINPAAMAKGLQDGMSSQLMTEQDKMVDVLFKQDLMAKRNAEF 114
QY 113 EKSKENLSLAEKFLKENSKNAGVVEVQPSKLYKIKKGAGKAISGKPSALLHYKGSFI 172
DB 115 SKKADENKSGEAFNLANKSKEGVSL-PSGLQYKILEKNGVKPSKDDTIVTVEYTGKLI 173
QY 173 NGQVSSSSGNNEPILLPLGQTIPGFALGMOGKEGTRVLYIHPDLAYG---TAGQLPP 229
DB 174 DGQVFDSTERTGTPATFKVSVQVIFGWTALQMLPAGSTWEIYIPSGLAYGPRSVGGPIGP 233
QY 230 NSLLIFEINLIQASADE 246
DB 234 NETLIFKIHLSVKKSD 250

RESULT 15
O32749
ID O32749 PRELIMINARY; PRT; 233 AA.
AC O32749;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Macrophage infectivity potentiator.
GN Name=miip;
OS Legionella birminghamensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.

```

```

OX NCBI_TaxID=28083;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43702;
RX MEDLINE=98010353; PubMed=9350870;
RA Ratcliff R.M., Donnellan S.C., Lanser J.A., Manning P.A.,
RA Heuzenroeder M.W.;
RT "Interspecies sequence differences in the Mip protein from the genus
RT Legionella; implications for function and evolutionary relatedness.";
RL Mol. Microbiol. 25:1149-1158 (1997).
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
DR EMBL; U91608; AAC45670.1; -
DR HSSP; P20380; 1FD9.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR008104; INFOTNTIATR.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR PRINTS; PR01730; INFOTNTIATR.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 233 AA; 24877 MW; 0297C61D08C41A32 CRC64;

Query Match 22.5%; Score 292.5; DB 2; Length 233;
Best Local Similarity 33.9%; Pred. No. 2.2e-12;
Matches 82; Conservative 36; Mismatches 89; Indels 35; Gaps 6;

QY 10 ATVALALSVASCDVRSKDKDQGSILVEYKDKNDNDIELS-DNOKLSRTFCHLLARQLR 68
DB 9 ATMGLAMSTATA-----ASDVTLSMDMDKLSYSGADLGRNFK 46
QY 69 KSEDMFFDIAEVAKQLAELVCKSAPLTETETEYEEKMAEVOK-----LVFEKSKENLS 121
DB 47 K-QGTEINPTAMAKGLQDGMSSQLMTEQDKMVDVLFKQDLMAKRNAEFSKSEENKA 105
QY 122 LAEKFLKENSKNAGVVEVQPSKLYKIKKGAGKAISGKPSALLHYKGSFINGQVFSSE 181
DB 106 KGTEFLSQKSKEGVSL-PSGLQYKIKIETGSGAKPAKDDTIVTVEYTGRTIDGQVFDSTD 164
QY 182 GNNEPILLPLGQTIPGFALGMOGKEGTRVLYIHPDLAYG---TAGQLPPNSLLIFEIN 238
DB 165 KSGKPAATFKVSVQVIFGWTALQMLPAGSTWEIYIPSGLAYGPRSVGGPIGPNETLIFKIH 224
QY 239 LI 240
DB 225 LI 226

Search completed: November 23, 2004, 12:18:24
Job time : 193 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: November 23, 2004, 12:10:53 ; Search time 40 Seconds  
(without alignments)  
620.598 Million cell updates/sec

Title: US-10-022-832-2  
Perfect score: 1299  
Sequence: 1 MNRWNVLATVALSAS.....LIQASDAVAAPQEGNQGE 258

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1299	100.0	258	2 F72052	peptidyl-prolyl ci
2	1299	100.0	258	2 B86573	fkbp-type peptidyl
3	763	58.7	243	2 S28638	probable fkbp-type
4	762	58.7	243	2 S25255	mip-like protein p
5	733	56.4	261	2 D81660	peptidyl-prolyl ci
6	297	22.9	272	2 C81068	macrophage infecti
7	287	22.1	272	2 D81800	probable peptidyl-
8	279	21.5	243	2 A43596	mip protein - Legi
9	274.5	21.1	233	2 S22665	mip protein - Legi
10	273.5	21.1	233	2 S57924	macrophage infecti
11	263	20.2	253	2 H83238	probable peptidyl-
12	244.5	18.8	177	2 B87700	peptidyl-prolyl ci
13	240.5	18.5	259	2 D82331	peptidyl-prolyl ci
14	235.5	18.1	264	2 F71272	probable peptidyl-
15	233.5	18.0	270	2 F91153	fkbp-type peptidyl
16	233.5	18.0	270	2 I65035	fkbp-type peptidyl
17	230.5	17.7	241	2 B84992	peptidylprolyl iso
18	228.5	17.6	266	2 AF0024	peptidylprolyl iso
19	228.5	17.6	270	2 B85999	hypothetical prote
20	223	17.2	241	2 A64155	hypothetical prote
21	221.5	17.1	272	2 AD1004	peptidylprolyl iso
22	219	16.9	205	2 F83075	peptidyl-prolyl ci
23	212.5	16.4	209	2 F82060	peptidyl-prolyl ci
24	211	16.2	157	2 C82431	peptidyl-prolyl ci
25	201.5	15.5	259	2 S56432	peptidylprolyl iso
26	201.5	15.5	259	2 A98277	hypothetical prote
27	192.5	14.8	259	2 A86118	hypothetical prote
28	186	14.3	244	2 F90126	hypothetical prote
29	186	14.3	295	2 B82659	peptidyl-prolyl ci

30	185	14.2	206	2 AE0429	peptidylprolyl iso
31	185	14.2	220	2 AE1053	peptidylprolyl iso
32	174	13.4	178	2 T44823	probable macrophag
33	170.5	13.1	487	2 T10215	hypothetical prote
34	167	12.9	457	2 JC5422	FK506-binding prot
35	166.5	12.8	152	2 B75347	peptidyl-prolyl ci
36	163	12.5	568	2 T06489	probable peptidylp
37	161.5	12.4	109	2 E82022	peptidylprolyl iso
38	161.5	12.4	109	2 F81245	FKBP-type peptidyl
39	161	12.4	165	2 AH1878	FKBP-type peptidyl
40	160.5	12.4	196	1 S55332	macrophage infecti
41	160	12.3	201	1 S75144	FKBP-type peptidyl
42	159	12.2	120	2 S11090	FK506-binding prot
43	159	12.2	361	2 T43536	peptidyl-prolyl ci
44	158	12.2	114	2 G87595	peptidyl-prolyl ci
45	156.5	12.0	551	1 S72485	peptidylprolyl iso

ALIGNMENTS

RESULT 1

F72052  
peptidyl-prolyl cis-trans isomerase Mip CP0086 [imported] - Chlamydoiphila pneumoniae (str: F72052)  
C:Species: Chlamydoiphila pneumoniae, Chlamydia pneumoniae  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: F72052; D81614  
R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999  
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A:Reference number: A72000; MUID:99206606; PMID:10192388  
A:Accession: F72052  
A:Molecule type: DNA  
A:Residues: 1-258 <ARN>  
A:Cross-references: UNIPROT:Q927P3; GB:AE001648; GB:AE001363; NID:G4376946; PIDN:AA18801  
A:Experimental source: strain CWL029  
R:Read, T.D.; Bruham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A:Reference number: A81500; MUID:20150255; PMID:10684935  
A:Accession: D81614  
A:Molecule type: DNA  
A:Residues: 1-258 <REA>  
A:Cross-references: GB:AE002172; GB:AE002161; NID:G7189018; PIDN:AAF37972.1; PID:G718902;  
A:Experimental source: strain AR39, HL cells  
C:Genetics:  
A:Gene: mip; CP0086  
C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl is F:160-205/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match		100.0%	Score 1299;	DB 2;	Length 258;
Best Local Similarity		100.0%;	Pred. No. 8.6e-84;		
Matches 258;		Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	1	MNRWNVLATVALSASCDVRSKDKQDQGSLSVEYKDKNDIELSNQKLSRTFG	60		
Db	1	MNRWNVLATVALSASCDVRSKDKQDQGSLSVEYKDKNDIELSNQKLSRTFG	60		
Qy	61	HLARQLRKSEDMFDIAEVAKGLQAEVLCKSAFLTETEEKMAEVQKLVFEKSKENL	120		
Db	61	HLARQLRKSEDMFDIAEVAKGLQAEVLCKSAFLTETEEKMAEVQKLVFEKSKENL	120		
Qy	121	SLAEKFLKENSKNAGVVEVQPSKLYKIIEKGAGKASGKPSALLHYKSGFINGQVFS	180		
Db	121	SLAEKFLKENSKNAGVVEVQPSKLYKIIEKGAGKASGKPSALLHYKSGFINGQVFS	180		
Qy	181	EGNNEPILLPLGQITPGFALGMQCKEGEIVYIHPDLAYGTAGQLPPNSLLIPEINLI	240		
Db	181	EGNNEPILLPLGQITPGFALGMQCKEGEIVYIHPDLAYGTAGQLPPNSLLIPEINLI	240		
Qy	241	QASADEVAAPQEGNQGE	258		
Db	241	QASADEVAAPQEGNQGE	258		



Qy 65 RQLRKSDFDIAEVAAGLQAEVLVCKSAPLTETETEYKMAEVLVQKLVFEKSKENLSLAE 124  
Db 57 RQLSRTEFSLDLVEVKGMSQSEIDGOSAPLTDTEYEQMAEVLQKAFKASCSNLSASAE 116  
Qy 125 KFLKSNKNAGVVEVQPSKQYKIIKEGAGKAISGKPSALLHYKGSFINGOVFSSEGN 184  
Db 117 EFLKENKEKAGVIELEPNKQYRVVKEGTGRVLSGKPTALLHYTGSDFGKVFOSSEKNK 176  
Qy 185 EPILLPLGQTTPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPPNSLLIFEINLIQASA 244  
Db 177 EPILLPLTKVTPGFSQMGQMGKEGVRVLYIHPDLAYGTAGQLPPNSLLIFEVVKLEAND 236  
Qy 245 DEVA 248  
Db 237 DNVS 240

## RESULT 5

peptidyl-prolyl cis-trans isomerase Mip TC0828 [imported] - Chlamydia muridarum (strain  
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn.  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 15-Jun-2001  
C:Accession: D81660  
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelber, J.F.; White, O.; Hickey,  
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A:Reference number: AB1500; MUID:20150255; PMID:10684935  
A:Accession: D81660  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-261 <TET>  
A:CROSS-references: GB:AB002349; GB:AE002160; NID:G7190851; PIDN:AAF39628.1; PID:G719085  
A:Experimental source: strain Nigg (MoPn)  
C:Genetics:  
A:Gene: TC0828  
A:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl i  
F:170-215/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 56.4%; Score 733; DB 2; Length 261;  
Best Local Similarity 59.4%; Pred. No. 3.5e-44;  
Matches 145; Conservative 35; Mismatches 54; Indels 10; Gaps 2;  
Qy 5 WNLVLATVALALSVCSDVRSKDKQDGSLVEYKDNKDTNDIELSDNQKLSRTFGHLLA 64  
Db 25 WNLMPF--AVALPILGC-----DNNGSGQTSAMGKDWVEDSVLTDNQKLSRTFGHLLA 74  
Qy 65 RQLRKSDFDIAEVAAGLQAEVLVCKSAPLTETETEYKMAEVLVQKLVFEKSKENLSLAE 124  
Db 75 RQLSSTEDFTLDTLTVIKGMSQSEIEBKSAPLTDSYETQMALVQKASFEKCSNLSASAE 134  
Qy 125 KFLKSNKNAGVVEVQPSKQYKIIKEGAGKAISGKPSALLHYKGSFINGOVFSSEGN 184  
Db 135 KFLKENKKEGVIELEPNKQYRVVKEGTGRVLTGKPNALLHYTGSDFGKVFDTSEKNK 194  
Qy 185 EPILLPLGQTTPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPPNSLLIFEINLIQASA 244  
Db 195 DPILLPLTKVTSFGSQMGQMGKEGVRVLYIHPDLAYGTSGQLPPNSLLIFEVVKLEAND 254  
Qy 245 DEVA 248  
Db 255 DNVS 258

## RESULT 6

C81068  
macrophage infectivity potentiator NMB1567 [imported] - Neisseria meningitidis (strain M  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: C81068  
R:Jettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.

Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: AB1000; MUID:20175755; PMID:10710307  
A:Accession: C81068  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-272 <TET>  
A:CROSS-references: UNIPROT:Q9JYI8; GB:AE002507; GB:AE002098; NID:G7226811; PIDN:AAF41921  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB1567  
A:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl i  
F:167-212/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 22.9%; Score 297; DB 2; Length 272;  
Best Local Similarity 31.8%; Pred. No. 1.2e-13;  
Matches 84; Conservative 42; Mismatches 124; Indels 14; Gaps 6;

Qy 1 MNRNWLVLATVALALSVCSDVRSKDKQDGSLVEYKDNKDTNDIELSDNQKLSRTFG 60  
Db 1 MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASAAQGDTSISG-STMQQASAYANG 59  
Qy 61 HLLARQLR--KSEDMFFDIAEVAAGLQAEVLVCKSAPLTETETEYKMAEVLVQKLVFEK 114  
Db 60 VDIGRSLKQMKEQGAIEDLVKVFTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAQKAVEK 119  
Qy 115 ---KSKENLSLAERFLKSNKNAGVVEVQPSKQYKIIKEGAGKAISGKPSALLHYKGSF 171  
Db 120 HKADAKANKEGEAFLEKNAKDG-VKTASGLQYKIKTKQEGKQPTKDDIVTVEYEGRL 178  
Qy 172 INGQVFSSEGNNEPILLGQTTPGFALGQMGKEGTRVLYIHPDLAY---GTAGQLP 228  
Db 179 IDGTVFDSSKANGGVPVFPPLSQVTPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIG 238  
Qy 229 PNSLLIFEINLIQASADEVAAPVQ 252  
Db 239 PNATLVDFVDKLVKIGAPENAPAKQ 262

## RESULT 7

DB1800  
probable peptidyl-prolyl isomerase NMA1756 [imported] - Neisseria meningitidis (strain Z  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C:Accession: D81800  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z491.  
A:Reference number: AB1775; MUID:20225556; PMID:10761919  
A:Accession: D81800  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-272 <PAR>  
A:CROSS-references: UNIPROT:Q9JUT0; GB:AL162757; GB:AL157959; NID:G7380371; PIDN:CAB84984  
A:Experimental source: serogroup A, strain Z491  
C:Genetics:  
A:Gene: NMA1756  
A:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl i  
F:167-212/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 22.1%; Score 287; DB 2; Length 272;  
Best Local Similarity 31.4%; Pred. No. 5.9e-13;  
Matches 83; Conservative 42; Mismatches 125; Indels 14; Gaps 6;

Qy 1 MNRNWLVLATVALALSVCSDVRSKDKQDGSLVEYKDNKDTNDIELSDNQKLSRTFG 60  
Db 1 MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASAAQGDTSISG-STMQQASAYANG 59  
Qy 61 HLLARQLR--KSEDMFFDIAEVAAGLQAEVLVCKSAPLTETETEYKMAEVLVQKLVFEK 114  
Db 60 VDIGRSLKQMKEQGAIEDLVKVFTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAQKAVEK 119

QY 115 ---KSKENLSLAEKFLKNSKNAGVVEQPSKLOYKIIKEGAGKAISGKPSALLHYKGSF 171  
Db 120 HKADAKANKGKGAFLKNAKDG-VKTASGLQYKTKGEGKQPTKDDIVVEGRL 178  
QY 172 INQVFSSESGNNEPILLPGITIPGALGQMGKEGTRVLYIHPDLAY---GTAGQLP 228  
Db 179 IDGTVFDSKANGPVTPLSPVLGTEGVLKKEGENTFVPSNLAVREQAGDKIG 238  
QY 229 PNLILFEINLIQASADEVAAPQ 252  
Db 239 PNATLVFVVKLVKIGAPENAPAKQ 262

RESULT 8  
A43596  
mip protein - Legionella micdadei  
C:Species: Legionella micdadei  
C>Date: 12-Jan-1993 #sequence\_revision 12-Jan-1993 #text\_change 09-Jul-2004  
C:Accession: A43596  
R:Bangborg, J.M.; Cianciotto, N.P.; Hinderson, P.  
Infect. Immun. 59, 3836-3840, 1991.  
A:Title: Nucleotide sequence analysis of the Legionella micdadei mip gene, encoding a 30  
A:Reference number: A43596; MUID:91373005; PMID:1840577  
A:Status: preliminary  
A:Accession: A43596  
A:Molecule type: DNA  
A:Residues: 1-243 <BAN>  
A:Cross-references: UNIPROT:P31106; GB:S62141; NID:G235621; PIDN:AAB19821.1; PID:G235622  
C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl  
F:153-198/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 21.5%; Score 279; DB 2; Length 243;  
Best Local Similarity 34.8%; Pred. No. 1.9e-12;  
Matches 72; Conservative 34; Mismatches 89; Indels 12; Gaps 4;

QY 50 SDNQLSRFTGHLLARQLKSEDMFFDIAEVAKGLQAEIVCKSAPIETEYEEKMAEVOK 109  
Db 38 TOTEKLSYSGADLGNFKK-QGIEISPAAMAKGLQDGMGGQLLLTDDQMKDVLNFKQ 96  
QY 110 -----LYPEKSKENLSLAEFLKNSKNAGVVEQPSKLOYKIIKEGAGKAISGKPS 162  
Db 97 DLMKKSASFNKKAEENKSGEAFLENKSKGWSL-PSGLQYNTILERGDGAKPTKDDV 155  
QY 163 ALLHYKGSFINGVFSSESGNNEPILLPGITIPGALGQMGKEGTRVLYIHPDLAYG 222  
Db 156 VIVEYTGKLDGQVFDSTKGTGPAFQSVQIPGTEALQMLPAGSTWEIYPSNLAYG 215  
QY 223 ---TAGQLPPNSLLIFEINLIQASADE 246  
Db 216 PRSVGGPIGNETLIFKIHLSVKKSD 242

RESULT 9  
S22665  
mip protein - Legionella pneumophila  
C:Species: Legionella pneumophila  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S22665; A30591  
R:Fischer, G.; Bang, H.; Ludwig, B.; Mann, K.; Hacker, J.  
Mol. Microbiol. 6, 1375-1383, 1992  
A:Title: Mip protein of Legionella pneumophila exhibits peptidyl-prolyl-cis/trans isomer  
A:Reference number: S22665; MUID:92349965; PMID:1739319  
A:Accession: S22665  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-233 <PIS>  
A:Cross-references: UNIPROT:Q93318; GB:S42595; NID:G252462; PIDN:AAB22717.1; PID:G252463  
R:Engleberg, N.C.; Carter, C.; Weber, D.R.; Cianciotto, N.P.; Eisenstein, B.I.  
Infect. Immun. 57, 1263-1270, 1989  
A:Title: DNA sequence of mip, a Legionella pneumophila gene associated with macrophage i  
A:Reference number: A30591; MUID:89173328; PMID:2925252  
A:Accession: A30591

A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-134, A', 136-233 <ENG>  
C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl i  
C:Keywords: membrane protein  
F:144-189/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 21.1%; Score 274.5; DB 2; Length 233;  
Best Local Similarity 32.0%; Pred. No. 3.6e-12;  
Matches 80; Conservative 35; Mismatches 98; Indels 37; Gaps 6;

QY 4 RNNVLATV---ALALSVASCDVRSKDKQOGSLVEYKDKNDTNDIELSDNQKLSRTFG 60  
Db 2 KMKLVTAAMGLAMSTAAATDTSLATDKD-----KLSYSTG 39

QY 61 HLLARQLKSEDMFFDIAEVAKGLQAEIVCKSAPIETEYEEKMAEVOK-----LVFE 113  
Db 40 ADLGNF-KNOGIDVNPAMAKGMDAMSGAQLALTEQOMKDVLNKFKDLMAKRTAEFN 98

QY 114 KSKENLSLAEFLKNSKNAGVVEQPSKLOYKIIKEGAGKAISGKPSALLHYKGSFN 173  
Db 99 KKAADENKVGAEFLTENKKNKPGV-VLPSGLQYKVINSGVGVKPSDVTVEYTGRLID 157

QY 174 GQVFSSESGNNEPILLPGITIPGALGQMGKEGTRVLYIHPDLAYG---TAGQLPN 230  
Db 158 GTVFDSTKGTGPAFQSVQIPGTEALQMLPAGSTWEIYVPSGLAYGPRSVGGPIGN 217

QY 231 SLLIFEINLI 240  
Db 218 ETLIFKIHLI 227

RESULT 10  
S57924

macrophage infectivity potentiator - Legionella longbeachae

N:Alternate names: mip protein

C:Species: Legionella longbeachae

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S57924

R:Doyle, R.M.; Manning, P.A.; Heuzenroeder, M.W.

submitted to the EMBL Data Library, November 1994

A:Description: Molecular characterization of the mip gene of Legionella longbeachae.

A:Reference number: S57924

A:Accession: S57924

A:Molecule type: DNA

A:Residues: 1-233 <DOY>

A:Cross-references: UNIPROT:P53605; EMBL:X83036; NID:G897774; PIDN:CAA58145.1; PID:G89777

A:Experimental source: ATCC 33462

C:Genetics:

A:Gene: mip

C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl i

C:Keywords: membrane protein

F:144-189/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 21.1%; Score 273.5; DB 2; Length 233;  
Best Local Similarity 30.8%; Pred. No. 4.3e-12;  
Matches 77; Conservative 42; Mismatches 94; Indels 37; Gaps 6;

QY 4 RNNVLATV---ALALSVASCDVRSKDKQOGSLVEYKDKNDTNDIELSDNQKLSRTFG 60  
Db 2 KMKLVTAAMGLAMSTAAATDTSLATDKD-----KLSYSTG 39

QY 61 HLLARQLKSEDMFFDIAEVAKGLQAEIVCKSAPIETEYEEKMAEVOK-----LVFE 113  
Db 40 ADLGNF-KNOGIDVNPVLAKGMDGMSGALILTEEQMKDVLSKFKDLMAKRTAEFN 98

QY 114 KSKENLSLAEFLKNSKNAGVVEQPSKLOYKIIKEGAGKAISGKPSALLHYKGSFN 173  
Db 99 KKAENKAKGDAFLSANKSKPGIV-VLPSGLQYKIIDAGTGAAPGKSDVTVEYTGRLID 157

QY 174 GQVFSSESGNNEPILLPGITIPGALGQMGKEGTRVLYIHPDLAYG---TAGQLPN 230  
Db 158 GTVFDSTKGTGPAFQSVQIPGTEALQMLPAGSTWEIYVPSGLAYGPRSVGGPIGN 217

Qy 231 SLLIFPINLI 240  
Best Local Similarity 31.6%, Pred. No. 2.6e-11; Length 253;  
Matches 77; Conservative 36; Mismatches 105; Indels 26; Gaps 5;  
Db 218 ETLIFKIHLI 227

RESULT 11  
H83238  
peptidyl-prolyl cis-trans isomerase, Fkbp-type PA3262 [imported] - Pseudomonas  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: H83238  
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bz  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: H83238  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-253 <STO>  
A:Cross-references: UNIPROT:Q9HYX8; GB:AE004748; GB:AE004091; NID:g9949378; PIDN:AAG0665  
C:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA3262  
C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl i

Query Match 20.2%, Score 263; DB 2; Length 253;  
Best Local Similarity 31.6%, Pred. No. 2.6e-11; Length 253;  
Matches 77; Conservative 36; Mismatches 105; Indels 26; Gaps 5;  
Db 3 RWNVLVATVALSVASCDVRSKDKDKDQGSLSVEYKDKNDTDELSDNKLSTFGHL 62  
2 KQHLRAIALVGLVSCDSQTN-----VELK-----TPAQKASVIGLN 42

Qy 63 LARQURKSEDMFFDIAEVAQGLQAEVLCKAPLTETEVEEKMAEVQKLVFEKKS---KEN 119  
Db 43 MGKLSIQSGMDLDSKAVAKGIEDALGKKQQLTDELTTEAFILQKRAERMAAIGDEN 102

Qy 120 LSLAEKFLKENSKNAGVVEQVPSKLOYYKIIKEGAKAISGPSALLHYKSGFINGOVSS 179  
Db 103 AKAGKKFLEENGKRGVTTASGLQYEVIVKADGPQPKATDVVTVHVEGRLTDGTVFDS 161

Qy 180 SEGNNPILLPLGQTIPGALGMOQKGEETRVLVIHPDLAYGT---AGQLPPNSLLIFE 236  
Db 162 SIERGSPIDLPSGVIPQWVEALQLMHVGEIKLYIPSELAYGAQSPSPAIPANSVLVFD 221

Qy 237 INLI 240  
Db 222 MELL 225

RESULT 12  
B87700  
peptidyl-prolyl cis-trans isomerase, FKBP-type [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: B87700  
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: B87700  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-177 <STO>  
A:Cross-references: UNIPROT:Q9A2C9; GB:AE005673; NID:gl13425390; PIDN:AAK25598.1; GSPDB:C  
C:Genetics:  
A:Gene: CC3636

Query Match 18.8%, Score 244.5; DB 2; Length 177;  
Best Local Similarity 38.1%, Pred. No. 3.3e-10; Length 177;  
Matches 51; Conservative 28; Mismatches 50; Indels 5; Gaps 3;  
Qy 114 KSKENLSLAEKFLKENSKNAGVVEQVPSKLOYYKIIKEG--AGKAISGPSALLHYKGSF 171  
Db 36 KKAQENLAADAFNAKNAKEFGVVTLP--PQGLQYKVRREGPNMGHPNKADEVKHYEGL 94

Qy 172 INGQVSSSEGNNEPILLPLGQTIPGALGMOQKGEETRVLVIHPDLAYGT--AGQLPP 229  
Db 95 IDGTVFDSSYERGVPAVFPDLGLVPAAWIALQRMKAGDEWILYVPPALGYGAQDKGPIPG 154

Qy 230 NSLLIFPINLIQAS 243  
Db 155 NSVMIFRIELDVN 168

RESULT 13  
D82331  
peptidyl-prolyl cis-trans isomerase, FKBP-type VC0354 [imported] - Vibrio cholerae (strai  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: D82331  
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.  
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: D82331  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-259 <HEI>  
A:Cross-references: UNIPROT:Q9KV04; GB:AE004124; GB:AE003852; NID:g9654770; PIDN:AAF93352;  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC0354  
A:Map position: 1  
C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl i

Query Match 18.5%, Score 240.5; DB 2; Length 259;  
Best Local Similarity 28.4%, Pred. No. 3.9e-10; Length 259;  
Matches 75; Conservative 48; Mismatches 108; Indels 33; Gaps 9;  
Qy 6 NLVATVALSVASCDVRSKDKDKD-----QGSLSVEYK--DNKOTNDIELSDNKL 56  
Db 8 SLLAATVTLAV--GCQKEAPKTETTPAAQTAAKTVEFKSEDDKAAVAIGVS----- 58

Qy 57 RTFGHLLARQURKSEDMFFDIAE--VAKGLQAEVLCKAPLTETE-----YEKMAEV 107  
Db 59 --FANYLKTSTIEKPSIEIGIDLNLKOLVLRKIE-HVFAGNPENMSEETRAALEALDKRVAET 115

Qy 108 QKLVFEKKSLENLSLAKEFLKENSKNAGVVEQVPSKLOYYKIIKEGAKAISGPSALLHY 167  
Db 116 MQAKAAEAKENKKGDGFRAQFEKESGVVKIQ--SGLLYQVMTPAEGDKPKDQTDVQVHY 174

Qy 168 KGSFINGQVSSSEGNNEPILLPLGQTIPGALGMOQKGEETRVLVIHPDLAYG--TAG 225  
Db 175 KGTLDIGSQFSSYERGERPATFPLNRVIPGVTGTEGVLMSVGSFKPLVIPPELAYGEQDTP 234

Qy 226 QLPNSLLIFPINLIQASDEVA 249  
Db 235 TIPANSTLVFVELLIENGKDA 258

RESULT 14  
F71272  
probable peptidyl-prolyl cis-trans isomerase, FKBP-type, 22 kDa (fklB) - syphilis spiroch  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: F71272  
R/Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDor

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-383, 1998  
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A:Reference number: A71250; MUID:98332770; PMID:9665876  
A:Accession: F71272  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-264 <COL>  
A:Cross-references: UNIPROT:O83834; GB:AE001256; GB:AE000520; NID:g3323171; PIDN:AAC6582  
A:Experimental source: strain Nichols  
C:Genetics:  
A:Gene: TP0862  
C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl  
F:173-216/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 18.1%; Score 235.5; DB 2; Length 264;  
Best Local Similarity 28.4%; Pred. No. 2.3e-09;  
Matches 73; Conservative 51; Mismatches 108; Indels 25; Gaps 9;  
QY 7 LVLATVALALSVASC-----DVRSKDKDQGSGLVEYKDKNDTNDIELSDNOK--LSR-- 57  
DB 16 LLLA-----GMSIFSCRKGAEGVSSAGEADKALT--ADQLDRKVQEQERQKTPLSKKS 69  
QY 58 ----TFGHLLARQLRKSEDMFFDIAEVAKGLQAEVCKSAPLTETVEEKKAEVQKLVFEK 114  
DB 70 VGYAFGLMGVTLQDSK-LDVLGQVWGLKTKVSADKDKQALADAQDVLQRAFEAYRQK 128  
QY 115 KSKENLSLAEKFLKENSKNAGVVEQVPSKLOYKIIKEGAKAISGPSALLHYKGSFING 174  
DB 129 EVEKKSQEAFLFEENAKKPG-VQVTSGLQYEVVVAADGPRQGGQRVTRTKGTLIDG 187  
QY 175 QVFSSEGNNEPILLPGQTIPGFALGQMCKEGEGRVLYIHPDLAY---GTAGQLPPNS 231  
DB 188 TVFDAS--RDKPAEPFDGMPGVSGSLKMPGVSTYRFVVPSSLGYGEGIEGVIPPCA 245  
QY 232 LLIFEINLIQASADEVA 248  
DB 246 LLVFEIQLQEIPLDSAS 262

RESULT 15  
F91153  
FKBP-type peptidyl-prolyl cis-trans isomerase [imported] - Escherichia coli (strain O157  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C:Accession: F91153  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: F91153  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-270 <HAY>  
A:Cross-references: UNIPROT:Q8X880; GB:BA000007; PIDN:BA837621.1; PID:g13363671; GSPDB:G  
A:Experimental source: strain O157:H7, substrain RIMD 050952  
C:Genetics:  
A:Gene: ECs4198  
C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl i

Query Match 18.0%; Score 233.5; DB 2; Length 270;  
Best Local Similarity 25.8%; Pred. No. 3.2e-09;  
Matches 71; Conservative 57; Mismatches 94; Indels 53; Gaps 9;  
QY 7 LVLATVALAL-----SVASCDVRSKDKDKDQ-----GSLVEYKDKNDTNDI 47  
DB 9 LIATTNAVALLHAPITFAEAAKPAATTADSKAFKDDQKSAVALGASLGRYMN----- 62  
QY 48 ELSDNQKLSRTFGHLLARQLRKSEDMFFDIAEVAKGLQAEVCKSAPLTETVEEKKAEV 107  
DB 63 SLKEQEKLG-----IKLDKDLIAGVQDAFADKS-KLSDQIEQLQAF 105

QY 108 QKLV-----PEKSKENLSLAEKFLKENSKNAGVVEQVPSKLOYKIIKEGAKAISGK 160  
DB 106 EAEVKSQAQKMEKDAADNEAKGEYREKFAKEG-VKTSSTGLVYQVVEAGKGEAPKDS 164  
QY 161 PSALLHYKGSFINGQVFSSEGNNEPILLPLGQTIPGFALGQMCKEGEGRVLYIHPDLA 220  
DB 165 DTVVNVYKGTLLIDGKEFDNSYTRGEPFLSFRLDGVIPTGWTEGLKNIKKGGKIKLVIPPELA 224  
QY 221 YGTAG--OLPNSNLLIFEINLIQAS-ADEVAAPQ 252  
DB 225 YGKAGVPGIPPNSTLVFDVVELLDVVKPAPKADAKPE 259

Search completed: November 23, 2004, 12:12:26  
Job time : 41 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 12:12:32 ; Search time 144 Seconds  
(without alignments)  
634.479 Million cell updates/sec

Title: US-10-022-832-2

Perfect score: 1299

Sequence: 1 MNRWNLVATVALSVA.....LIQSADEVAAPVQGNQGE 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1299	100.0	258	14	US-10-022-832-2
2	1299	100.0	258	15	US-10-312-273-55
3	1299	100.0	258	15	US-10-289-762-699
4	233	17.9	537	14	US-10-179-038-8
5	226	17.4	239	11	US-09-809-665A-143
6	194	14.9	390	14	US-10-369-493-10319
7	180.5	13.9	585	16	US-10-437-963-158013
8	178.5	13.7	344	15	US-10-425-114-68360
9	171	13.2	553	14	US-10-310-154-496
10	170.5	13.1	495	17	US-10-425-115-323715
11	169	13.0	314	16	US-10-767-701-45023
12	168	12.9	230	14	US-10-369-493-8922
13	168	12.9	505	15	US-10-424-599-160002

14	168	12.9	544	15	US-10-424-599-174536	Sequence 174536,
15	167	12.9	147	17	US-10-425-115-185116	Sequence 185116,
16	166.5	12.8	152	14	US-10-369-493-631	Sequence 631, App
17	166.5	12.8	601	16	US-10-437-963-141440	Sequence 141440,
18	161.5	12.4	588	17	US-10-425-115-367862	Sequence 367862,
19	159	12.2	107	9	US-09-751-100B-69	Sequence 69, Appl
20	159	12.2	107	9	US-09-751-100B-83	Sequence 83, Appl
21	158.5	12.2	634	17	US-10-425-115-210281	Sequence 210281,
22	156.5	12.0	410	15	US-10-425-114-51083	Sequence 51083, A
23	155.5	12.0	363	14	US-10-270-223-6	Sequence 6, Appl
24	153	11.8	327	16	US-10-408-765A-422	Sequence 422, App
25	151.5	11.7	134	17	US-10-425-115-268186	Sequence 268186,
26	151	11.6	548	15	US-10-424-599-223790	Sequence 223790,
27	150.5	11.6	230	14	US-10-341-967-111	Sequence 111, App
28	150	11.5	107	9	US-09-751-100B-82	Sequence 82, Appl
29	149.5	11.5	137	14	US-10-341-967-85	Sequence 85, Appl
30	149	11.5	483	14	US-10-270-223-2	Sequence 2, Appl
31	146.5	11.3	185	17	US-10-425-115-210428	Sequence 210428,
32	143.5	11.0	139	14	US-10-369-493-6160	Sequence 6160, Ap
33	143	11.0	107	9	US-09-751-100B-67	Sequence 67, Appl
34	143	11.0	107	9	US-09-751-100B-80	Sequence 80, Appl
35	143	11.0	108	10	US-09-970-561-4	Sequence 4, Appl
36	143	11.0	108	14	US-10-024-298A-121	Sequence 121, App
37	143	11.0	108	14	US-10-042-211A-121	Sequence 121, App
38	143	11.0	108	15	US-10-617-217A-121	Sequence 121, App
39	143	11.0	108	17	US-10-024-298A-121	Sequence 121, App
40	143	11.0	127	14	US-10-341-967-40	Sequence 40, Appl
41	143	11.0	127	14	US-10-341-967-72	Sequence 72, Appl
42	143	11.0	128	9	US-09-781-804-21	Sequence 21, Appl
43	143	11.0	128	15	US-10-716-062-21	Sequence 21, Appl
44	143	11.0	144	9	US-09-925-299-985	Sequence 985, App
45	143	11.0	144	10	US-09-925-299-985	Sequence 985, App

#### ALIGNMENTS

RESULT 1  
US-10-022-832-2  
; Sequence 2, Application US/10022832  
; Publication No. US20030059896A1  
; GENERAL INFORMATION:  
; APPLICANT: COUTURE, FRANCE  
; APPLICANT: HAMEL, JOSEF  
; APPLICANT: BRODEUR, BERNARD R.  
; APPLICANT: MARTIN, DENIS  
; TITLE OF INVENTION: NOVEL CHLAMYDIA ANTIGENS AND CORRESPONDING DNA  
; FILE OF INVENTION: FRAGMENTS  
; FILE REFERENCE: BIOVAC-15  
; CURRENT APPLICATION NUMBER: US/10/022.832  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/256,941  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-10-022-832-2

Query Match	100.0%	Score 1299;	DB 14;	Length 258;
Best Local Similarity	100.0%;	Pred. No. 8e-109;		
Matches 258;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	MNRWNLVATVALSVA	CDVRSKDKDQGS	LVVEYKONKDTNDIELSNQKLSRTFG 60
Db	1	MNRWNLVATVALSVA	CDVRSKDKDQGS	LVVEYKONKDTNDIELSNQKLSRTFG 60
Qy	61	HLARQLRKSEDMFDDIAE	VAQELVCKSA	PLTETETEYEKMAEVOKLVPEKKS KENL 120
Db	61	HLARQLRKSEDMFDDIAE	VAQELVCKSA	PLTETETEYEKMAEVOKLVPEKKS KENL 120

QY 121 SLAEKFLKSNAGVVEVQPSKLYKIIKEGAGKAIKSGPALLHYKGSFINGQVFSSS 180  
DB 121 SLAEKFLKSNAGVVEVQPSKLYKIIKEGAGKAIKSGPALLHYKGSFINGQVFSSS 180  
QY 181 EGNNEPILLPLGQTIPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPNSLLIFEINLI 240  
DB 181 EGNNEPILLPLGQTIPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPNSLLIFEINLI 240  
QY 241 QASADEVAAPQEGNOGE 258  
DB 241 QASADEVAAPQEGNOGE 258

## RESULT 2

US-10-312-273-55  
; Sequence 55, Application US/10312273  
; Publication No. US20040005667A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE  
; FILE REFERENCE: P025035W0  
; CURRENT APPLICATION NUMBER: US/10/312,273  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: 0016363.4  
; PRIOR FILING DATE: 2000-07-03  
; PRIOR APPLICATION NUMBER: 0017047.2  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 0017983.8  
; PRIOR FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: 0019368.0  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: 0020440.4  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: 0022583.9  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 0027549.5  
; PRIOR FILING DATE: 2000-11-10  
; PRIOR APPLICATION NUMBER: 0031706.5  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 664  
; SOFTWARE: Seqwin99, version 1.02  
; SEQ ID NO 55  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-10-312-273-55

Query Match 100.0%; Score 1299; DB 15; Length 258;  
Best Local Similarity 100.0%; Pred. No. 8e-109;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNRRLNLVATVALSALSVASCDVRSKDKDQGSVLEYKDKNDTNDIELSDNQLSRTFG 60  
DB 1 MNRRLNLVATVALSALSVASCDVRSKDKDQGSVLEYKDKNDTNDIELSDNQLSRTFG 60  
QY 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVPEKSKENL 120  
DB 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVPEKSKENL 120  
QY 121 SLAEKFLKSNAGVVEVQPSKLYKIIKEGAGKAIKSGPALLHYKGSFINGQVFSSS 180  
DB 121 SLAEKFLKSNAGVVEVQPSKLYKIIKEGAGKAIKSGPALLHYKGSFINGQVFSSS 180  
QY 181 EGNNEPILLPLGQTIPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPNSLLIFEINLI 240  
DB 181 EGNNEPILLPLGQTIPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPNSLLIFEINLI 240  
QY 241 QASADEVAAPQEGNOGE 258  
DB 241 QASADEVAAPQEGNOGE 258

## RESULT 3

Query Match 17.9%; Score 233; DB 14; Length 537;  
Best Local Similarity 28.3%; Pred. No. 3.7e-12;  
Matches 62; Conservative 53; Mismatches 86; Indels 18; Gaps 7;

US-10-289-762-699  
; Sequence 699, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 699  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-10-289-762-699

Query Match 100.0%; Score 1299; DB 15; Length 258;  
Best Local Similarity 100.0%; Pred. No. 8e-109;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNRRLNLVATVALSALSVASCDVRSKDKDQGSVLEYKDKNDTNDIELSDNQLSRTFG 60  
DB 1 MNRRLNLVATVALSALSVASCDVRSKDKDQGSVLEYKDKNDTNDIELSDNQLSRTFG 60  
QY 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVPEKSKENL 120  
DB 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVPEKSKENL 120  
QY 121 SLAEKFLKSNAGVVEVQPSKLYKIIKEGAGKAIKSGPALLHYKGSFINGQVFSSS 180  
DB 121 SLAEKFLKSNAGVVEVQPSKLYKIIKEGAGKAIKSGPALLHYKGSFINGQVFSSS 180  
QY 181 EGNNEPILLPLGQTIPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPNSLLIFEINLI 240  
DB 181 EGNNEPILLPLGQTIPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPNSLLIFEINLI 240  
QY 241 QASADEVAAPQEGNOGE 258  
DB 241 QASADEVAAPQEGNOGE 258

## RESULT 4

US-10-179-038-8  
; Sequence 8, Application US/10179038  
; Publication No. US20030096352A1  
; GENERAL INFORMATION:  
; Sequenzprotokoll  
; APPLICANT: Roche Diagnostics GmbH  
; APPLICANT: F. Hoffmann-La Roche AG  
; TITLE OF INVENTION: Use of FKBP chaperones as expression tool  
; FILE REFERENCE: 21306W0  
; CURRENT APPLICATION NUMBER: US/10/179,038  
; CURRENT FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: EP01115225.3  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: EP01120939.2  
; PRIOR FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 537  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: single-chain  
; OTHER INFORMATION: FKBP  
US-10-179-038-8

RESULT 6  
US-10-369-493-10319  
; Sequence 10319, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xiaofeng

```

Query Match      13.9%; Score 180.5; DB 16; Length 585;
Best Local Similarity 30.6%; Pred. No. 2.3e-07;
Matches 53; Conservative 34; Mismatches 63; Indels 23; Gaps 7;

Qy 101 EEKMAEQKLVFEKKSKENSLAEKFLKENSNNAGVVEQPSKLOYKIIKEGAG--KAIS 158
Db 15 EEEVDVNMKDEBDESSDSSPVAMKVGEEK-----EIGKQRLKRLKKEGWDWPES 67

```

```
QY 159 GKPSALLHYKSGFINGQVSSSEGNNEPILLPLGQ--TIPGFALGMQMKGEGETRVLYIH 216
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 G-DEVQVHYTGTLDDGKFPSSRRDGTTPFKFSLGQGEVINGWDEGIKTKMKGQAVFTVP 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 217 PDLAYTAGO---LPNSLLIFINLIQ-ASADEVA-----AVPQEGNQGE 258
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 PELAYGEAGSPAIPNATLRFDEVELLSWASVKDICKDGGIFPKKVLAEHGKWE 179
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-10-425-114-68360
; Sequence 68360, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68360
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZWELMOL17161C02_FLI.pap
US-10-425-114-68360

Query Match 13.7%; Score 178.5; DB 15; Length 344;
Best Local Similarity 26.8%; Pred. No. 1.6e-07;
Matches 63; Conservative 39; Mismatches 98; Indels 35; Gaps 8;

QY 24 RSKDKDKQGSLEY-KDKNDTNDIELSDNQKLSRTFGHLLARQLRKSDEMPFDIAEVAK 82
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 KKKKGKDKSTVMDTKVKNKEEVKHQSDPADPASTKHKKKKNKNKS-----ASG 174
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 83 GLQAEVLCKSPALTEYEKEKMAEVQKLVPEKK-----SKENLSLAEKFLKEN---- 130
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 GDTSEQSAKNNDKNEEASAEANKKKNKKAHDI SRSESQAGTGLGESDSKEPLQTR 234
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 131 ---SKNAGVVEQPSKLYKIIKEGAGKAISGKPSALLHYKSGFINGQVSSS-EGNNEPI 187
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 TFANGNMIOEVENMGKPDGK--KASRGKKVS-----VRYIGKLKNGTIFDSNVNGRPF 286
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 188 LPLGQTIPCFALGMQMKGEGETRVLYIHPDLAYGT--AGOLPPNSLLIFEINLI 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 287 RLGVGVISGDVGVNGMRVGDKRRLLTIPPSMGYGRVGGQIQFQNSTLIFDELV 341
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-10-310-154-496
; Sequence 496, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
```

```
; APPLICANT: Dong, Jinzhao
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine L.
; APPLICANT: Miller, Philip W.
; APPLICANT: Padmavathi, Manchikanti
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Start, William G.
; APPLICANT: Tennesen, Dan
; APPLICANT: Vidya, K.R.
; APPLICANT: Wang, Haiyun
; APPLICANT: Xin, Zhanquo
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Yajuan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15(52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 496
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Zea mays
US-10-310-154-496

Query Match 13.2%; Score 171; DB 14; Length 553;
Best Local Similarity 36.7%; Pred. No. 1.5e-06;
Matches 40; Conservative 20; Mismatches 43; Indels 6; Gaps 3;

QY 138 EVQPSKLYKIIKEGAG-KAISGKPSALLHYKSGFINGQVSSSEGNNEPILLPL--GOT 194
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 39 EVKGEGLKKLKEGEGWETPEVGDEVEHYTGTLDDGKFPSSRRDGEFFKFKLGGQV 98
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 195 IPGFALGMQMKGEGETRVLYIHPDLAYTAGO---LPNSLLIFEINLI 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 99 IKGWDQGIKTKMKKGENAFTIPPELAYGASGSPPTIPNATLQFDVELL 147
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-10-425-115-323715
; Sequence 323715, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
```



